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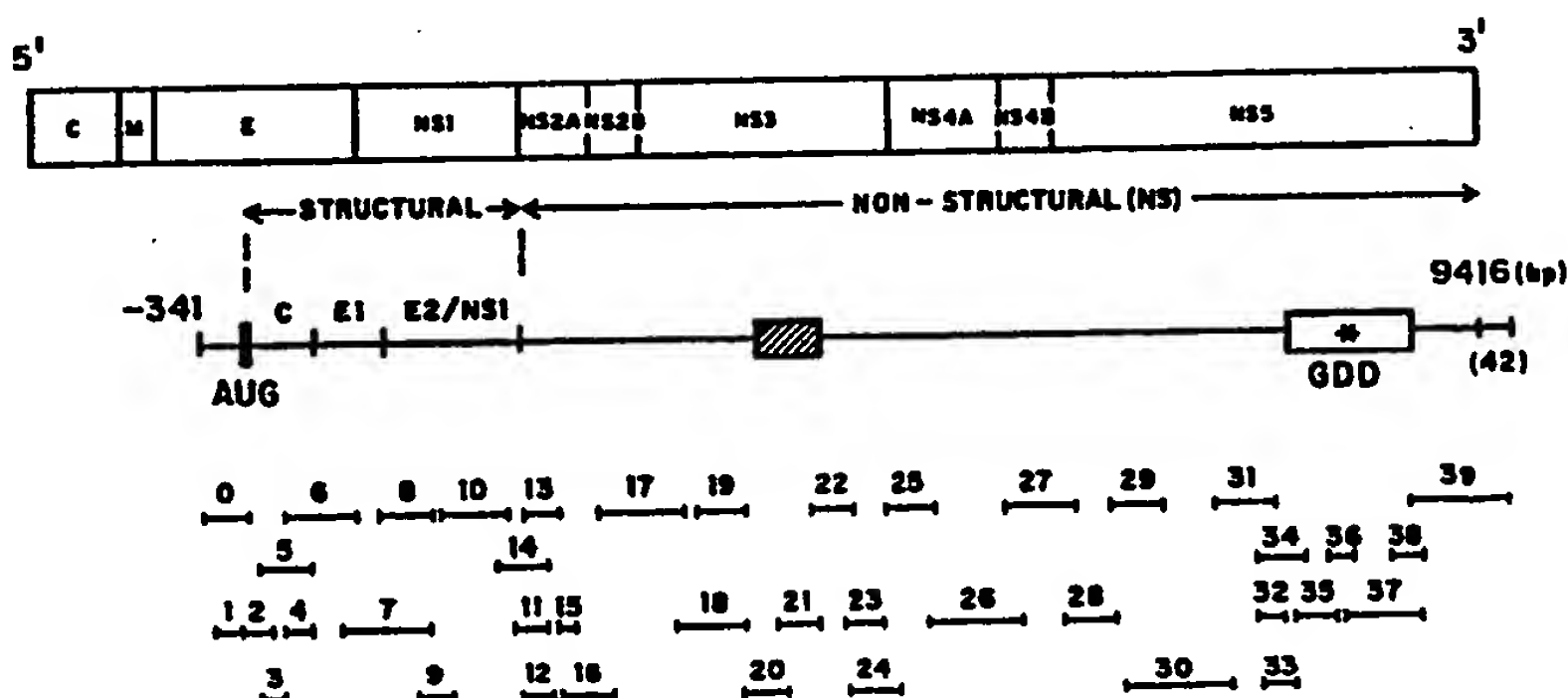
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(54) Title: NON-A, NON-B HEPATITIS VIRUS ANTIGEN, DIAGNOSTIC METHODS AND VACCINES

Flaviviruses
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= NS3 dengue type 2
 = replicase CARMV

(57) Abstract

The present invention relates to a DNA segment encoding a recombinant non-A, non-B hepatitis structural protein or fusion protein and a recombinant DNA (rDNA) molecule capable of expressing either protein. Cells transformed with the rDNA, methods for producing the proteins in addition to compositions containing the proteins, and their use in diagnostic methods and systems, and in vaccines are also described.

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NON-A, NON-B HEPATITIS VIRUS ANTIGEN,
DIAGNOSTIC METHODS AND VACCINES

Description

5 Technical Field

The present invention relates to a segment of deoxyribonucleic acid (DNA) that encodes a non-A, non-B hepatitis structural protein and a recombinant DNA (rDNA) that contains the DNA segment. Cells transformed with a rDNA of the present invention and methods for producing the NANBV structural protein are also contemplated. The invention also describes compositions containing a NANBV structural protein useful in diagnostic methods and in vaccines.

15

Background of the Invention

Non-A, non-B hepatitis (NANBH) is believed to be caused by a transmissible virus that has been referred to as both hepatitis C virus (HCV) and non-A, non-B hepatitis virus (NANBV). Although the transmissible disease was discovered years ago, a complete characterization of the causative agent is still being developed.

Isolates of NANBV have been obtained and portions or all of the viral genome of the various isolates were molecularly cloned and sequenced. Choo et al, Science, 244:359-362 (1989); Choo et al., Proc. Natl. Acad. Sci. USA, 88:2451-2455 (1991); Takamizawa et al., J. Virol., 65:1105-1113 (1991); Kato et al., Proc. Natl. Acad. Sci. USA, 87:9524-9528 (1990); and Takeuchi et al., Nucl. Acids Res., 18:4626 (1990). Similarities in nucleotide base sequence between the different isolates of NANBV suggest that they are a part of a family of related viruses. Okamoto et al, Japan J. Exp. Med., 60:163-177 (1990); and Ogata et al., Proc. Natl. Acad. Sci. USA, 88:3392-3396 (1991).

Properties of the NANBV genome suggest that NANBV may be a very distant relative of the flavivirus family. However, similarities in both the size and hydropathicity of the structural proteins suggest that
5 NANB viruses may also be distantly related to the pestivirus family. Miller et al., Proc. Natl. Acad. Sci., 87:2057-2061 (1990); and Okamoto et al., Japan J. Exp. Med., 60:163-177 (1990).

10 The difficulties in characterizing the NANBV isolates taxonomically and the lack of information regarding the proteins encoded by the NANBV genome have made it difficult to identify relevant gene products useful for diagnostic markers and for producing NANBV vaccines.

15 The NANBV genome is comprised of a positive stranded RNA molecule that codes for a single polyprotein. The gene products of NANBV are believed to include both structural and nonstructural proteins, based on homologies to characterized, related viruses.
20 From these homologies, it is predicted that NANBV expresses a single polyprotein gene product from the complete viral genome, which is then cleaved into functionally distinct structural and nonstructural proteins. This type of viral morphogenesis precludes
25 positive identification of the individual mature viral proteins until they have been physically isolated and characterized. Since no in vitro culturing system to propagate the virus has been developed for NANBV, no NANBV structural or nonstructural gene products
30 (proteins) have been isolated from biological specimens or NANBV-infected cells. Thus, the identification of NANBV proteins, of their role in the viral life cycle, and of their role in disease, have yet to be determined. In particular, antigenic markers

for NANBV-induced disease have yet to be fully characterized.

One NANBV gene product, namely the antigen C100-3, derived from portions of the nonstructural genes designated NS3 and NS4, has been expressed as a fusion protein and used to detect anti-C100-3 antibodies in patients with various forms of NANB hepatitis. See, for example, Kuo et al, Science, 244:362-364 (1989); and International Application No. PCT/US88/04125. A diagnostic assay based on C100-3 antigen is commercially available from Ortho Diagnostics, Inc. (Raritan, NJ). This C100-3 assay currently represents the state of the art in detecting NANBV infections. However, the C100-3 antigen-based immunoassay has been reported to preferentially detect antibodies in sera from chronically infected patients. C100-3 seroconversion generally occurs from four to six months after the onset of hepatitis, and in some cases C100-3 fails to detect any antibody where an NANBV infection is present. Alter et al., New Eng. J. Med., 321:1538-39 (1989); Alter et al., New Eng. J. Med., 321:1494-1500 (1989); and Weiner et al., Lancet, 335:1-3 (1990). McFarlane et al., Lancet, 335:754-757 (1990), described false positive results when the C100-3-based immunoassay was used to measure antibodies in patients with autoimmune chronic active hepatitis. Using the C100-3-based immunoassay, Grey et al., Lancet, 335:609-610 (1990), describe false positive results on sera from patients with liver disease caused by a variety of conditions other than NANBV.

A NANBV immunoassay that could accurately detect seroconversion at early times after infection, or that could identify an acute NANBV infection, is not presently available.

The Hutch strain of HCV is a clinically interesting isolate compared to the Donn strain (HCV-1) because HCV-H grows to extremely high titers in the patient.

5

Summary of the Invention

One Hutch strain (HCV-H) of non-A, non-B hepatitis virus (NANBV) designated the Hutch c59 isolate (or HCV-Hc59) has been propagated through
10 passage in animals and the entire viral genome has been cloned and sequenced. When using the term "subgroup" the present specification refers to a group of NANBVs which is serologically defined by particular strains, such as the Hutch c59 strain. Sequence data
15 shows differences at both the nucleotide and amino acid level when compared to previously reported NANBV strains. See, the sequences of the following HCV isolates, where the isolate designation is shown in parenthesis for comparison, Okamoto et al, Japan J. Exp. Med., 60:163-177, 1990 (HC-J1, HC-J4); Takeuchi
20 et al., Nucleic Acids Res., 18:4626, 1990 (HCV-JH); Choo et al., Proc. Natl. Acad. Sci. USA, 88:2451-2455, 1991 (HCV-1); Kato et al., Proc. Natl. Acad. Sci. USA, 87:9524-9528, 1990 (HCV-J); Takamizawa et al., J. Virol., 65:1105-1113, 1991 (HCV-BK); United States
25 Patent No. 5,032,511 to Takahashi et al.; Ogata et al., Proc. Natl. Acad. Sci. USA, 88:3392-3396, 1991 (HCV-Hh); and International Application No. PCT/US88/04125.

30 The identified sequences have been shown herein to encode structural proteins of NANBV. The NANBV structural proteins are also shown herein to include antigenic epitopes useful for diagnosis of antibodies immunoreactive with structural proteins of NANBV, and
35 for use in vaccines to induce neutralizing antibodies

against NANBV. In particular, the NANBV antigens of this invention are Hutch c59 isolate NANBV antigens.

5 The nucleotide sequence that codes for the amino terminal polyprotein portion of the structural genes of the Hutch strain of NANBV is contained in SEQ ID NO:1. By comparison to other NANBV isolates, to flavivirus, and to pestivirus, the nucleotide sequence contained in SEQ ID NO:1 is believed to encode structural proteins of NANBV, namely capsid and
10 portions of envelope.

The structural antigens described herein are present in the putative capsid protein contained in SEQ ID NO:1 from amino acid residue positions 1-120, and are present in the amino terminal portion of the
15 putative envelope protein contained in SEQ ID NO:1 from residue positions 121 to 326.

Nucleotide and amino acid residue sequences are defined herein from a starting base or amino acid residue position number to an end base or residue
20 position number. It is understood that all such sequences include both the starting and end position numbers.

The complete sequence of the genome of the Hutch c59 isolate has also been determined and is described.
25 Thus, the present invention contemplates a DNA segment encoding the viral genome of the Hutch c59 isolate of NANBV contained in SEQ ID NO:46 from nucleotide position 1 to 9416.

The present invention also contemplates a DNA
30 segment encoding a NANBV structural protein that comprises a NANBV structural antigen, preferably capsid antigen. A particularly preferred capsid antigen includes an amino acid residue sequence represented by SEQ ID NO:1 from residue 1 to residue
35 20, from residue 21 to residue 40, from residue 2 to

residue 40, or from residue 1 to residue 74, and the DNA segment preferably includes the nucleotide base sequence represented by SEQ ID NO:1 from base position 1 to base position 60, from base position 61 to base position 120, from base position 4 to base position 120, or from base position 1 to base position 222, respectively.

A polynucleotide is also contemplated comprising a nucleotide sequence that encodes portions of the Hutch c59 isolate polyprotein, particularly portions of the sequence-specific regions of c59 in the V, V₁, V₂ or V₃ region.

Also contemplated is a recombinant DNA molecule comprising a vector, preferably an expression vector, operatively linked to a DNA segment of the present invention. A preferred recombinant DNA molecule is pGEX-3X-690:691, pGEX-3X-690:694, pGEX-3X-693:691, pGEX-3X-15:17, pGEX-3X-15:18, pGEX-2T-15:17, pGEX-2T-CAP-A, pGEX-2T-CAP-B or pGEX-2T-CAP-A-B.

A NANBV structural protein is contemplated that comprises an amino acid residue sequence that defines a NANBV structural antigen, preferably a capsid antigen, and more preferably one that includes the amino acid residue sequence contained in SEQ ID NO:1 from residue 1 to residue 20, from residue 21 to residue 40, from residue 2 to residue 40, or from residue 1 to residue 74. Fusion proteins comprising a NANBV structural protein of this invention are also contemplated.

The invention also contemplates an antibody containing antibody molecules that immunoreact with the Hutch c59 isolate of NANBV, but do not immunoreact with NANBV isolates HCV-1, HCV-BK, HCV-J, HC-J1, HC-J4, HCV-JH or HCV-Hh, i.e., c59-specific antibody molecules.

Further contemplated is a culture of cells transformed with a recombinant DNA molecule of this invention and methods of producing a NANBV structural protein of this invention using the culture.

5 Also contemplated is a composition comprising a NANBV structural protein. The composition is preferably characterized as being essentially free of (a) procaryotic antigens, and (b) other NANBV-related proteins.

10 Still further contemplated is a diagnostic system in kit form comprising, in an amount sufficient to perform at least one assay, a NANBV structural protein composition, a polypeptide or a fusion protein of this invention, as a separately packaged reagent.

15 Preferably, the diagnostic system contains the fusion protein affixed to a solid matrix.

Further contemplated is a method, preferably an in vitro method, of assaying a body fluid sample for the presence of antibodies against at least one of the
20 NANBV structural antigens described herein. The method comprises forming an immunoreaction admixture by admixing (contacting) the body fluid sample with an immunological reagent such as a NANBV structural protein, polypeptide or fusion protein of this
25 invention. The immunoreaction admixture is maintained for a time period sufficient for any of the antibodies present to immunoreact with the admixed immunological reagent to form an immunoreaction product, which product, when detected, is indicative of the presence
30 of anti-NANBV structural protein antibodies.

Preferably, the immunological reagent is affixed to a solid matrix when practicing the method.

The invention also contemplates a method, preferably an in vitro method, of assaying a body
35 sample for the presence of NANBV polynucleic acids.

The method generally comprises a) forming an aqueous hybridization admixture by admixing a body sample with an polynucleotide of this invention; b) maintaining the aqueous hybridization admixture for a time period and under hybridizing conditions sufficient for any NANBV polynucleic acids present in the body sample to hybridize with the admixed polynucleotides to form a hybridization product; and c) detecting the presence of any of the hybridization product formed and thereby the presence of NANBV polynucleic acids in the body sample.

In another embodiment, this invention contemplates an inoculum (or a vaccine) comprising an immunologically effective amount of a NANBV structural protein, polypeptide or fusion protein of this invention dispersed in a pharmaceutically acceptable carrier and/or diluent. The inoculum is essentially free of (a) procaryotic antigens, and (b) other NANBV-related proteins.

A prophylactic method for treating infection, which method comprises administering an inoculum of the present invention, is also contemplated.

Brief Description of the Drawings

Figure 1 is a schematic representation of the HCV-Hc59 genome and location of HCV-Hc59 cDNA clones numbered from zero to 39. Alignment with the protein encoded by flaviviruses is shown as well as the putative domains in the HCV encoded genome. Regions of amino acid homology with the Dengue Type 2 Ns3 virus and the Carnation Mottle virus (CARMv) are indicated by striped and empty boxes, respectively.

Detailed Description of the InventionA. Definitions

Amino Acid: All amino acid residues identified herein are in the natural L-configuration. In keeping with standard polypeptide nomenclature, J. Biol. Chem., 243:3557-59, (1969), abbreviations for amino acid residues are as shown in the following Table of Correspondence:

TABLE OF CORRESPONDENCE		
10	<u>SYMBOL</u>	<u>AMINO ACID</u>
	<u>3-Letter</u>	
	Tyr	L-tyrosine
	Gly	L-glycine
	Phe	L-phenylalanine
15	Met	L-methionine
	Ala	L-alanine
	Ser	L-serine
	Ile	L-isoleucine
	Leu	L-leucine
20	Thr	L-threonine
	Val	L-valine
	Pro	L-proline
	Lys	L-lysine
	His	L-histidine
25	Gln	L-glutamine
	Glu	L-glutamic acid
	Glx	Gln or Glu
	Trp	L-tryptophan
	Arg	L-arginine
30	Asp	L-aspartic acid
	Asn	L-asparagine
	Asx	Asp or Asn
	Cys	L-cysteine
35	Xaa	Unknown or other

It should be noted that all amino acid residue sequences, typically referred to herein as "residue sequences", are represented herein by formulae whose left to right orientation is in the conventional direction of amino-terminus to carboxy-terminus.

5 Antigen: A polypeptide or protein that is able to specifically bind to (immunoreact with) an antibody and form an immunoreaction product (immunocomplex). The site on the antigen with which the antibody binds is referred to as an antigenic determinant or epitope.

10 Nucleotide: a monomeric unit of DNA or RNA consisting of a sugar moiety (pentose), a phosphate, and a nitrogenous heterocyclic base. The base is linked to the sugar moiety via the glycosidic carbon (1' carbon of the pentose) and that combination of base and sugar is a nucleoside. When the nucleoside contains a phosphate group bonded to the 3' or 5' position of the pentose it is referred to as a nucleotide. A sequence of operatively linked

15 nucleotides is typically referred to herein as a "base sequence", and is represented herein by a formula whose left to right orientation is in the conventional direction of 5'-terminus to 3'-terminus.

20 Duplex DNA: A double-stranded nucleic acid molecule comprising two strands of substantially complementary polynucleotide hybridized together by the formation of a hydrogen bond between each of the complementary nucleotides present in a base pair of the duplex. Because the nucleotides that form a base pair can be either a ribonucleotide base or a

25 deoxyribonucleotide base, the phrase "duplex DNA" refers to either a DNA-DNA duplex comprising two DNA strands (ds DNA), or an RNA-DNA duplex comprising one DNA and one RNA strand.

30

Base Pair (bp): a partnership of adenine (A) with thymine (T), or of cytosine (C) with guanine (G) in a double stranded DNA molecule. In RNA, uracil (U) is substituted for thymine.

5 Complementary Nucleotide Sequence: a sequence of nucleotides in a single-stranded molecule of DNA or RNA that is sufficiently complementary to that on another single strand to specifically (non-randomly) hybridize to it with consequent hydrogen bonding.

10 Hybridization: the pairing of complementary nucleotide sequences (strands of nucleic acid) to form a duplex, heteroduplex or complex containing more than two single-stranded nucleic acids by the establishment of hydrogen bonds between/among complementary base
15 pairs. It is a specific, i.e. non-random, interaction between/among complementary polynucleotides that can be competitively inhibited.

Hybridization Product: The product formed when a polynucleotide hybridizes to a single or double-
20 stranded nucleic acid. When a polynucleotide hybridizes to a double-stranded nucleic acid, the hybridization product formed is referred to as a triple helix or triple-stranded nucleic acid molecule. Moser et al, Science, 238:645-50 (1987).

25 Nucleotide Analog: a purine or pyrimidine nucleotide that differs structurally from a A, T, G, C, or U, but is sufficiently similar to substitute for the normal nucleotide in a nucleic acid molecule. Inosine (I) is a nucleotide that can hydrogen bond
30 with any of the other nucleotides, A, T, G, C, or U. In addition, methylated bases are known that can participate in nucleic acid hybridization.

B. DNA Segments

 In living organisms, the amino acid residue
35 sequence of a protein or polypeptide is directly

related via the genetic code to the deoxyribonucleic acid (DNA) sequence of the structural gene that codes for the protein. Thus, a structural gene can be defined in terms of the amino acid residue sequence, i.e., protein or polypeptide, for which it codes.

An important and well known feature of the genetic code is its redundancy. That is, for most of the amino acids used to make proteins, more than one coding nucleotide triplet (codon) can code for or designate a particular amino acid residue. Therefore, a number of different nucleotide sequences may code for a particular amino acid residue sequence. Such nucleotide sequences are considered functionally equivalent since they can result in the production of the same amino acid residue sequence in all organisms. Occasionally, a methylated variant of a purine or pyrimidine may be incorporated into a given nucleotide sequence. However, such methylations do not affect the coding relationship in any way.

In one embodiment the present invention contemplates an isolated DNA segment that comprises a nucleotide base sequence that encodes a NANBV structural protein comprising a NANBV structural antigen such as a capsid antigen, an envelope antigen, or both. Preferably, the structural antigen is immunologically related to the Hutch strain of NANBV.

More preferably, the encoded NANBV structural antigen has an amino acid residue sequence that corresponds, and preferably is identical, to the amino acid residue sequence contained in SEQ ID NO:1.

In one embodiment, the putative capsid antigen includes an amino acid residue sequence contained in SEQ ID NO:1 from residue 1 to residue 20, from residue 21 to residue 40, from residue 2 to residue 40, or from residue 1 to residue 74. In another embodiment,

the capsid antigen includes the sequence contained in SEQ ID NO:1 from residue 69 to residue 120.

In another embodiment, the putative envelope antigen includes an amino acid residue sequence
5 contained in SEQ ID NO:1 from residue 121 to residue 176 or from residue 121 to residue 326.

Preferred DNA segments include a base sequence represented by the base sequence contained in SEQ ID NO:1 from base position 1 to base position 222, from
10 base position 205 to base position 360, from base position 361 to base position 528, or from base position 361 to base position 978.

In preferred embodiments, the length of the nucleotide base sequence is no more than about 3,000
15 bases, preferably no more than about 1,000 bases.

The amino acid residue sequence of a particularly preferred NANBV structural protein is contained in SEQ ID NO:2 from residue 1 to residue 315, in SEQ ID NO:3 from residue 1 to residue 252, in SEQ ID NO:4 from
20 residue 1 to residue 252 and in SEQ ID NO:6 from residue 1 to residue 271.

A purified DNA segment of this invention is substantially free of other nucleic acids that do not contain the nucleotide base sequences specified herein
25 for a DNA segment of this invention, whether the DNA segment is present in the form of a composition containing the purified DNA segment, or as a solution suspension or particulate formulation. By substantially free is meant that the DNA segment is
30 present as at least 10% of the total nucleic acid present by weight, preferably greater than 50 percent, and more preferably greater than 90 percent of the total nucleic acid by weight.

In another embodiment, a DNA segment of this
35 invention contains a nucleotide base sequence that

defines a structural gene capable of expressing a fusion protein. The phrase "fusion protein" refers to a protein having a polypeptide portion operatively linked by a peptide bond to a second polypeptide portion defining a NANBV structural antigen as disclosed herein.

A preferred first polypeptide portion has an amino acid residue sequence corresponding to a sequence as contained in SEQ ID NO:2 from about residue 1 to about residue 221, and is derived from the protein glutathione-S-transferase (GST).

A preferred second polypeptide portion defining a NANBV structural antigen in a fusion protein includes an amino acid residue sequence represented by the sequence contained in SEQ ID NO:1 from residue 1 to residue 20, from residue 21 to residue 40, from residue 2 to residue 40, from residue 1 to residue 74, from residue 69 to residue 120, from residue 121 to residue 176, or from residue 121 to residue 326.

In one embodiment, a fusion protein can contain more than one polypeptide portion defining a NANBV structural antigen, as for example the combination of two polypeptide portions representing different structural antigens as shown by the amino acid residue sequence contained in SEQ ID NO:1 from residue 1 to residue 120, or in SEQ ID NO:1 from residue 1 to residue 326.

In particularly preferred embodiments, that portion of a fusion protein encoding DNA segment of this invention that codes for the polypeptide portion defining a NANBV capsid antigen includes a nucleotide base sequence corresponding to a sequence that codes for an amino acid residue sequence as contained in SEQ ID NO:1 from residue 1 to residue 20, from residue 21 to residue 40, from residue 2 to residue 40, or from

residue 1 to residue 74, and more preferably includes a nucleotide base sequence corresponding to a base sequence as contained in SEQ ID NO:1 from base 1 to base 60, from base 61 to base 120, from base 4 to base 120, or from base 1 to base 222, respectively.

In another embodiment, that portion of a fusion protein encoding DNA segment of this invention that codes for the polypeptide portion defining a NANBV envelope antigen includes a nucleotide base sequence corresponding to a sequence that codes for an amino acid residue sequence as contained in SEQ ID NO:1 from residue 121 to residue 176 or from residue 121 to residue 326, and more preferably includes a nucleotide base segment corresponding in base sequence to the nucleotide base sequence contained in SEQ ID NO:1 from base 361 to base 528 or from base 361 to base 978, respectively.

A particularly preferred fusion protein encoding DNA segment of this invention has a nucleotide base sequence corresponding to the sequence contained in SEQ ID NO:2 from base 1 to base 945, SEQ ID NO:3 from base 1 to base 756, SEQ ID NO:4 from base 1 to base 756, and SEQ ID NO:6 from base 1 to base 813.

In preferred embodiments, a DNA segment of the present invention is bound to a complementary DNA segment, thereby forming a double stranded DNA segment. In addition, it should be noted that a double stranded DNA segment of this invention preferably has a single stranded cohesive tail at one or both of its termini.

In another embodiment, a DNA segment of the present invention comprises a nucleotide base sequence that encodes the genome of the Hutch isolate of NANBV. Preferably, the DNA segment has a nucleotide base sequence that encodes the amino acid residue sequence

of the polyprotein produced by the genome of the Hutch c59 isolate, which amino acid residue sequence is shown in SEQ ID NO:46 from residue 1 to residue 3011. More preferably, the DNA segment in this embodiment
5 has the nucleotide sequence shown in SEQ ID NO:46 from base 1 to base 9416.

A DNA segment encoding the c59 isolate genome is useful for the preparation of a hybridization standard or control in diagnostic methods based on nucleic acid
10 hybridization using the polynucleotides, for the preparation of NANBV structural antigens or fusion proteins by recombinant DNA methods, for the preparation of infectious NANBV c59 isolate particles in culture, and the like, all of which are described
15 herein.

In another embodiment, the present invention contemplates a fragment of a DNA segment of this invention corresponding to a portion of a NANBV genome or encoding a portion of a NANBV structural antigen.
20 These fragments, when present in single stranded form or specified in the context of one strand of a double stranded DNA segment, are referred to herein as polynucleotides.

Where the polynucleotide is used to encode a
25 NANBV structural antigen, or region of the Hutch c59 isolate polyprotein, the polynucleotide corresponds to the coding strand of a NANBV genome as described herein. Where the polynucleotide is used as a
hybridization probe or primer for hybridization with
30 NANBV-derived nucleic acids, the sense of the strand will depend, as is well known upon the target sequence to which hybridization is directed.

Thus in one embodiment, the present invention contemplates a polynucleotide that comprises a
35 nucleotide base sequence that includes a nucleotide

base sequence that encodes an amino acid residue sequence corresponding to a portion of the polyprotein expressed by the Hutch isolate of NANBV. Preferably the polynucleotide encodes a sequence that corresponds to a portion of the amino acid residue sequence of the c59 isolate shown in SEQ ID NO:46 from residue 1 to residue 3011.

Particularly preferred are regions of the Hutch c59 isolate which are unique and thereby provide a means to distinguish the Hutch isolate, and more preferably the c59 isolate, from other isolates of NANBV on the basis of amino acid residue or nucleotide base sequence differences. Regions of the genome of the c59 isolate useful for distinguishing isolates contain differences in nucleotide base sequence, and preferably define differences in the encoded amino acid residue sequence, when compared to the nucleotide or amino acid residue sequence of the isolate to be distinguished.

Representative comparisons to identify Hutch isolate sequence differences are shown herein in the Examples, and particularly in Table 11.

Thus, a polynucleotide of this invention in one embodiment comprises a nucleotide base sequence that includes a nucleotide sequence that encodes an amino acid residue sequence that corresponds to a portion of the sequence of the Hutch c59 isolate of NANBV shown in SEQ ID NO:46 such that the polynucleotide has at least one nucleotide base difference in sequence when compared to the nucleotide sequence of a strain of NANBV selected from the group consisting of HCV-1, HCV-BK, HCV-J, HC-J1, HC-J4, HCV-JH and HCV-Hh. Preferably the nucleotide base sequence includes a sequence defining a portion of the variable region of the NANBV genome selected from the group consisting

of: the V variable region nucleotide base sequence (base 1497 to base 1574 of SEQ ID NO:46), the V₁ variable region nucleotide base sequence (base 1077 to base 1166 of SEQ ID NO:46), the V₂ variable region nucleotide base sequence (base 1707 to base 1787 of SEQ ID NO:46), and the V₃ variable region nucleotide base sequence (base 7407 to base 7478 of SEQ ID NO:46).

The SEQ ID NO and corresponding bases of the sequence are referred to herein conveniently in parenthesis following a reference to a sequence. For example, the sequence of nucleotides from base 1 to base 9416 shown in SEQ ID NO:46 is referred to as "46:1-9416".

Particularly preferred polynucleotides have a nucleotide base sequence selected from the group consisting of the V variable region nucleotide base sequence (46:1497-1574), the V₁ variable region nucleotide base sequence (46:1077-1166), the V₂ variable region nucleotide base sequence (46:1707-1787), and the V₃ variable region nucleotide base sequence (46:7407-7478).

In another embodiment, a polynucleotide comprises a nucleotide base sequence that includes a nucleotide sequence that encodes an amino acid residue sequence selected from the group consisting of residue 391 to residue 404 of SEQ ID NO:46, residue 246 to residue 256 of SEQ ID NO:46, residue 461 to residue 466 of SEQ ID NO:466, residue 473 to residue 482 of SEQ ID NO:46, and residue 2356 to residue 2379 of SEQ ID NO:46.

Preferably, the included nucleotide sequence corresponds to the sequence shown in SEQ ID NO:46. The above-indicated ranges of amino acid residues correspond to portions of the V, V₁, V₂ and V₃ regions that contain the greatest amount of sequence diversity

when compared to known HCV isolates, and therefore are most preferred.

For reasons of ease of synthesis and sequence specificity, preferred polynucleotides are from about
5 10 to about 200 nucleotides in length, although the particular length will depend upon the purpose for using the polynucleotide.

A polynucleotide for use in the present invention in its various embodiments includes a primer, a probe,
10 or a nucleic acid.

The term "probe" as used herein refers to a polynucleotide, whether purified from a nucleic acid restriction digest or produced synthetically, which is
15 about 8 to 200 nucleotides in length, having a nucleotide base sequence that is substantially complementary to a predetermined specific nucleic acid sequence present in a gene of interest, i.e. a target nucleic acid.

The polynucleotide probe must be sufficiently
20 long to be capable of hybridizing under hybridizing conditions with a specific nucleic acid sequence present in the gene of interest. The exact length of the polynucleotide probe will depend on many factors, including hybridization temperature and the nucleotide
25 sequence of the probe. For example, depending on the complexity of the target sequence, a polynucleotide probe typically contains 15 to 25 or more nucleotides, although it can contain fewer nucleotides. As few as
30 8 nucleotides in a polynucleotide have been reported as effective for use. Studier et al, Proc. Natl. Acad. Sci. USA, 86:6917-21 (1989). Short polynucleotide probes generally require lower temperatures to form sufficiently stable hybrid complexes with target 5.

In preferred embodiments a polynucleotide probe has a size of less than about 200 nucleotides in length, preferably less than 100 nucleotides, and more preferably less than 30 nucleotides.

5 By "substantially complementary" and its grammatical equivalents in relation to a probe is meant that there is sufficient nucleotide base sequence similarity between a subject polynucleotide probe and a specific nucleic acid sequence present in
10 a gene of interest that the probe is capable of hybridizing with the specific sequence under hybridizing conditions and form a duplex comprised of the probe and the specific sequence.

Therefore, the polynucleotide probe sequence may
15 not reflect the exact sequence of the target sequence so long as the probe contains substantial complementarity with the target sequence. For example, a non-complementary polynucleotide can be attached to the one end of the probe, with the
20 remainder of the probe sequence being substantially complementary to the target sequence. Such non-complementary polynucleotides might code for an endonuclease restriction site or a site for protein binding. Alternatively, non-complementary bases or
25 longer sequences can be interspersed into the probe, provided the probe sequence has sufficient complementarity with the sequence of the target strand as to non-randomly hybridize therewith and thereby form a hybridization product under hybridization
30 conditions.

The polynucleotide probe is provided in single-stranded form for maximum efficiency, but may alternatively be double stranded. If double stranded, the polynucleotide probe is first treated to separate
35 its strands before being used in hybridization to

prepare hybridization products. Preferably, the probe is a polydeoxyribonucleotide.

5 A DNA segment or polynucleotide of the present invention can easily be prepared from isolated virus obtained from the blood of a NANBV-infected individual such as described herein or can be synthesized de novo by chemical techniques.

10 De novo chemical synthesis of a DNA segment or a polynucleotide can be conducted using any suitable method, such as, for example, the phosphotriester or phosphodiester methods. See Narang et al., Meth. Enzymol., 68:90, (1979); U.S. Patent No. 4,356,270; Itakura et al., Ann. Rev. Biochem., 53:323-56 (1989); Brown et al., Meth. Enzymol., 68:109, (1979); and
15 Matteucci et al., J. Am. Chem. Soc., 103:3185 (1981). (The disclosures of the art cited herein are incorporated herein by reference.) Of course, by chemically synthesizing the structural gene portion, any desired modifications can be made simply by
20 substituting the appropriate bases for those encoding a native amino acid residue. However, DNA segments including sequences identical to a segment contained in SEQ ID NOS 1, 2, 3, 4 or 6 are preferred.

25 Derivation of a polynucleotide from nucleic acids involves the cloning of a nucleic acid into an appropriate host by means of a cloning vector, replication of the vector and therefore multiplication of the amount of the cloned nucleic acid, and then the isolation of subfragments of the cloned nucleic acids.
30 For a description of subcloning nucleic acid fragments, see Maniatis et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, pp 390-401 (1982); and see U.S. Patents No. 4,416,988 and No. 4,403,036.

In addition, a DNA segment can be prepared by first synthesizing oligonucleotides that correspond to portions of the DNA segment, which oligonucleotides are then assembled by hybridization and ligation into a complete DNA segment. Such methods are also well known in the art. See for example, Paterson et al., Cell, 48:441-452 (1987); and Lindley et al., Proc. Natl. Acad. Sci., 85:9199-9203 (1988), where a recombinant peptide, neutrophil-activated factor, was produced from the expression of a chemically synthesized gene in E. coli.

A DNA segment of this invention can be used for the preparation of rDNA molecules, in the construction of vectors for expressing a NANBV structural protein or fusion protein of this invention, or as a hybridization probe for detecting the presence of NANBV specific nucleic acid sequences in samples.

Where the use of a DNA segment is for preparing proteins, the specified amino acid residue is considered important, and the nucleotide base sequence of the DNA segment can vary based on the redundancy of the genetic code, as is well known, to provide for the desired amino acid residue sequence.

Where the use of a DNA segment is as a hybridization probe for specific nucleic acid sequences, it is a nucleotide base sequence corresponding to the Hutch strain NANBV nucleotide base sequences disclosed herein that is preferred.

C. Recombinant DNA Molecules

The present invention further contemplates a recombinant DNA (rDNA) that includes a DNA segment of the present invention operatively linked to a vector. A preferred rDNA of the present invention is characterized as being capable of directly expressing, in a compatible host, a NANBV structural protein or

fusion protein of this invention. Preferred DNA segments for use in a rDNA are those described herein above.

By "directly expressing" is meant that the mature polypeptide chain of the protein is formed by translation alone as opposed to proteolytic cleavage of two or more terminal amino acid residues from a larger translated precursor protein. Preferred rDNAs of the present invention are the plasmids pGEX-3X-690:694 , pGEX-3X-693:691, pGEX-3X-690:691, pGEX-3X-15:17, pGEX-3X-15:18, pGEX-2T-15:17, pGEX-2T-CAP-A, pGEX-2T-CAP-B, and pGEX-2T-CAP-A-B described in Example 1.

A recombinant DNA molecule (rDNA) of the present invention can be produced by operatively linking a vector to a DNA segment of the present invention. Exemplary rDNA molecules and the methods for their preparation are described in Example 1.

In another embodiment, a rDNA molecule of this invention comprises a vector operatively linked to a DNA segment comprising a nucleotide base sequence that encodes the genome of the Hutch isolate of NANBV. Preferably, the rDNA molecule includes a nucleotide base sequence that encodes the amino acid residue sequence of the polyprotein produced by the genome of the Hutch c59 isolate, which amino acid residue sequence is shown in SEQ ID NO:46 from residue 1 to residue 3011. More preferably, the rDNA molecule in this embodiment includes a nucleotide base sequence shown in SEQ ID NO:46 from base 1 to base 9416.

As used herein, the term "vector" refers to a DNA molecule capable of autonomous replication in a cell and to which another DNA segment can be operatively linked so as to bring about replication of the attached segment. Typical vectors are plasmids,

bacteriophages and the like. Vectors capable of directing the expression of a NANBV structural protein or fusion protein are referred to herein as "expression vectors". Thus, a recombinant DNA molecule (rDNA) is a hybrid DNA molecule comprising at least two nucleotide sequences not normally found together in nature.

The choice of vector to which a DNA segment of the present invention is operatively linked depends directly, as is well known in the art, on the functional properties desired, e.g., protein expression, and the host cell to be transformed, these being limitations inherent in the art of constructing recombinant DNA molecules. However, a vector contemplated by the present invention is at least capable of directing the replication, and preferably also expression, of the recombinant or fusion protein structural gene included in DNA segments to which it is operatively linked.

In preferred embodiments, a vector contemplated by the present invention includes a procaryotic replicon (ori); i.e., a DNA sequence having the ability to direct autonomous replication and maintenance of the recombinant DNA molecule extrachromosomally in a procaryotic host cell, such as a bacterial host cell, transformed therewith. Such replicons are well known in the art. In addition, those embodiments that include a procaryotic replicon also typically include a gene whose expression confers drug resistance to a bacterial host transformed therewith. Typical bacterial drug resistance genes for use in these vectors are those that confer resistance to ampicillin or tetracycline. Typical of such vector plasmids are pUC8, pUC9, pBR322 and pBR329 available from Biorad Laboratories, (Richmond, CA).

Those vectors that include a procaryotic replicon can also include a procaryotic promoter capable of directing the expression (transcription and translation) of the gene encoding a NANBV structural protein or fusion protein in a bacterial host cell, such as E. coli, transformed therewith. A promoter is an expression control element formed by a DNA sequence that permits binding of RNA polymerase and subsequent transcription initiation to occur. Promoter sequences compatible with bacterial hosts are typically provided in plasmid vectors containing convenient restriction sites for insertion of a DNA segment of the present invention. A typical vector is pPL-lambda available from Pharmacia, (Piscataway, NJ).

Vector plasmids having a bacterial promoter that is inducible with IPTG are the pTTQ plasmids available from Amersham (Arlington Heights, IL), and the pKK223-3 plasmid available from Pharmacia. Additional expression vectors for producing in procaryotes a cloned gene product in the form of a fusion protein are well known and commercially available.

Although the expression vectors pGEX-3X and pGEX-2T have been used as exemplary in producing the fusion proteins described herein, other functionally equivalent expression vectors can be used.

Functionally equivalent vectors contain an expression promoter that is inducible by IPTG for fusion protein expression in E. coli, and a configuration such that upon insertion of the DNA segment into the vector a fusion protein is produced. Commercially available vectors functionally equivalent to the vectors pGEX-3X and pGEX-2T used herein include the pGEMEX-1 plasmid vector from Promega (Madison, WI) that produces a fusion between the amino terminal portion of the T7 gene 10 protein and the cloned insert gene, the pMAL

plasmid vectors from New England Biolabs (Beverly, MA) that produce a fusion with the maltose binding protein (MBP) encoded by the mal E gene, and the pGEX-3X and pGEX-2T plasmids from Pharmacia that produce a fusion with the enzyme glutathione-s-transferase (GST) and the cloned insert gene, respectively.

The construction and use of the pGEX-3X and pGEX-2T vectors have been described by Smith et al., Gene, 67:31-40 (1988), which reference is hereby incorporated by reference.

In particularly preferred embodiments, a fusion protein contains a GST derived polypeptide-portion as an added functional domain operatively linked to a NANBV structural antigen of this invention. Any inducible promoter driven vector, such as the vectors pTTQ, pKK223-3, pGEX-3X or pGEX-2T described above and the like, can be used to express a GST-NANBV structural protein, referred to herein as a GST:NANBV fusion protein. Thus, although the pGEX-3X and pGEX-2T vectors are described as exemplary, the DNA molecules of this invention are not to be construed as limited to these vectors, because the invention in one embodiment is directed to an rDNA for expression of a protein having NANBV structural antigens fused to GST and not drawn to the vector per se.

A variety of methods have been developed to operatively link DNA segments to vectors via complementary cohesive termini. For instance, complementary homopolymer tracts can be added to the DNA segment to be inserted and to the vector DNA. The vector and DNA segment are then joined by hydrogen bonding between the complementary homopolymeric tails to form recombinant DNA molecules.

Synthetic linkers containing one or more restriction sites provide an alternative method of

joining the DNA segment to vectors. A DNA segment generated by endonuclease restriction digestion is treated with bacteriophage T4 DNA polymerase or E. coli DNA polymerase I, enzymes that remove protruding, 3', single-stranded termini with their 3'-5' exonucleolytic activities and fill in recessed 3' ends with their polymerizing activities.

The combination of these activities therefore generates blunt-ended DNA segments. The blunt-ended segments are then incubated with a large molar excess of linker molecules in the presence of an enzyme that is able to catalyze the ligation of blunt-ended DNA molecules, such as bacteriophage T4 DNA ligase. Thus, the products of the reaction are DNA segments carrying polymeric linker sequences at their ends. These DNA segments are then cleaved with the appropriate restriction enzyme and ligated to an expression vector that has been cleaved with an enzyme that produces termini compatible with those of the DNA segment.

Synthetic linkers containing a variety of restriction endonuclease sites are commercially available from a number of sources including International Biotechnologies, Inc., New Haven, CN.

Also contemplated by the present invention are RNA equivalents of the above described recombinant DNA molecules.

D. Transformed Cells and Cultures

The present invention also relates to a host cell transformed with a recombinant DNA molecule of the present invention. The term "host cell" includes both eukaryotic and prokaryotic hosts. Preferred rDNA molecules for use in a transformed cell are those described herein above and preferably are rDNAs capable of expressing a recombinant or fusion protein. Specific preferred embodiments of transformed cells

are those which contain an rDNA molecule having one of the preferred DNA segments described herein above, and particularly cells transformed with the rDNA plasmid pGEX-3X-690:694, pGEX-3X-693:691, pGEX-3X-690:691, pGEX-3X-15:17, pGEX-3X-15:18, pGEX-2T-15:17, pGEX-2T-CAP-A, pGEX-2T-CAP-B, or pGEX-2T-CAP-A-B.

Bacterial cells are preferred procaryotic host cells and typically are a strain of E. coli, such as, for example, the E. coli strain DH5 available from Bethesda Research Laboratories, Inc., Bethesda, MD. Transformation of appropriate cell hosts with a recombinant DNA molecule of the present invention is accomplished by well known methods that typically depend on the type of vector used. With regard to transformation of procaryotic host cells, see, for example, Cohen et al., Proc. Natl. Acad. Sci. USA, 69:2110 (1972); and Sambrook et al., Molecular Cloning, A Laboratory Manual, 2nd Ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, NY (1989).

Successfully transformed cells, i.e., cells that contain a recombinant DNA molecule of the present invention, can be identified by well known techniques. For example, cells resulting from the introduction of an rDNA of the present invention can be isolated as single colonies. Cells from those colonies can be harvested, lysed and their DNA content examined for the presence of the rDNA using a method such as that described by Southern, J. Mol. Biol., 98:503 (1975) or Berent et al., Biotech., 3:208 (1985).

In addition to directly assaying for the presence of rDNA, cells transformed with the appropriate rDNA can be identified by well known immunological methods when the rDNA is capable of directing the expression of a NANBV structural protein. For example, cells successfully transformed with an expression vector of

this invention produce proteins displaying NANBV structural protein antigenicity. Samples of cells suspected of being transformed are harvested and assayed for the presence of a NANBV structural antigen using antibodies specific for that antigen, such
5 antibodies being described further herein.

Thus, in addition to the transformed host cells themselves, the present invention also contemplates a culture of those cells, preferably a monoclonal
10 (clonally homogeneous) culture, or a culture derived from a monoclonal culture, in a nutrient medium. Preferably, the culture also contains a protein displaying NANBV structural protein antigenicity.

Nutrient media useful for culturing transformed
15 host cells are well known in the art and can be obtained from several commercial sources.

E. Methods for Producing NANBV Structural Proteins, Polypeptides and Fusion Proteins

Another aspect of the present invention
20 pertains to a method for producing recombinant proteins and fusion proteins of this invention.

The present method entails initiating a culture comprising a nutrient medium containing host cells, preferably E. coli cells, transformed with a
25 recombinant DNA molecule of the present invention that is capable of expressing a NANBV structural protein or a fusion protein. The culture is maintained for a time period sufficient for the transformed cells to express the NANBV structural protein or fusion
30 protein. The expressed protein is then recovered from the culture.

Expression vectors and expression vector culturing conditions for producing NANBV structural proteins are generally well known in the art. Such
35 vectors and culturing conditions can be altered

without affecting the spirit of the present invention. However, preferred are the vectors designed specifically for the production of proteins not normally found in the host cell used to express a NANBV structural protein. Exemplary are the vectors that contain inducible promoters for directing the expression of DNA segments that encode the NANBV structural protein. Vectors with promoters inducible by IPTG are also well known. See for example plasmids PTTQ and pKK223-3 available from Amersham and Pharmacia respectively. Particularly preferred are the promoters inducible by IPTG present in the pGEX vectors pGEX-3X and pGEX-2T described herein.

Using vectors with inducible promoters, expression of NANBV structural proteins requires an induction phase at the beginning of the above described maintenance step for expressing the protein, as is known and described in detail in Example 2.

Methods for recovering an expressed protein from a culture are well known in the art and include fractionation of the protein-containing portion of the culture using well known biochemical techniques. For instance, the methods of gel filtration, gel chromatography, ultrafiltration, electrophoresis, ion exchange, affinity chromatography and the like, such as are known for protein fractionations, can be used to isolate the expressed proteins found in the culture. In addition, immunochemical methods, such as immunoaffinity, immunoadsorption and the like can be performed using well known methods.

Particularly preferred are isolation methods that utilize the presence of the polypeptide portion defining glutathione-S-transferase (GST) as a means to separate the fusion protein from complex mixtures of protein. Affinity adsorption of a GST-containing

fusion protein to a solid phase containing glutathione affixed thereto can be accomplished as described by Smith et al., Gene, 67:31 (1988). Alternatively, the GST-containing polypeptide portion of the fusion protein can be separated from the NANBV structural antigen by selective cleavage of the fusion protein at a specific proteolytic cleavage site, according to the methods of Smith et al., Gene, 67:31 (1988). Exemplary isolation methods are described in Examples 5 and 6.

In addition to its preparation by the use of a rDNA expression vector, a NANBV structural protein comprising a NANBV structural antigen can be prepared in the form of a synthetic polypeptide.

Polypeptides can be synthesized by any of the techniques that are known to those skilled in the polypeptide art. Synthetic chemistry techniques, such as a solid-phase Merrifield-type synthesis, are preferred for reasons of purity, antigenic specificity, freedom from undesired side products, ease of production and the like, and can be carried out according to the methods described in Merrifield et al., J. Am. Chem. Soc., 85:2149-2154 (1963) and Houghten et al., Int. J. Pept. Prot. Res., 16:311-320 (1980). An excellent summary of the many techniques available can be found in J.M. Steward and J.D. Young, "Solid Phase Peptide Synthesis", W.H. Freeman Co., San Francisco, 1969; M. Bodanszky, et al., "Peptide Synthesis", John Wiley & Sons, Second Edition, 1976 and J. Meienhofer, "Hormonal Proteins and Peptides", Vol. 2, p. 46, Academic Press (NY), 1983 for solid phase peptide synthesis, and E. Schroder and K. Kubke, "The peptides", Vol. 1, Academic Press (New York), 1965 for classical solution synthesis, each of which is incorporated herein by reference.

Appropriate protective groups usable in such synthesis are described in the above texts and in J.F.W. McOmie, "Protective Groups in Organic Chemistry", Plenum Press, New York, 1973, which is
5 incorporated herein by reference.

A subject polypeptide includes any chemical derivative of a polypeptide whose amino acid residue sequence is shown herein. Therefore, a present polypeptide can be subject to various changes where
10 such changes provide for certain advantages in its use.

"Chemical derivative" refers to a subject polypeptide having one or more residues chemically derivatized by reaction of a functional side group.
15 Such derivatized molecules include for example, those molecules in which free amino groups have been derivatized to form amine hydrochlorides, p-toluene sulfonyl groups, carbobenzoxy groups, t-butyloxycarbonyl groups, chloroacetyl groups or
20 formyl groups. Free carboxyl groups may be derivatized to form salts, methyl and ethyl esters or other types of esters or hydrazides. Free hydroxyl groups may be derivatized to form O-acyl or O-alkyl derivatives. The imidazole nitrogen of histidine may
25 be derivatized to form N-im-benzylhistidine. Also included as chemical derivatives are those peptides which contain one or more naturally occurring amino acid derivatives of the twenty standard amino acids. For examples: 4-hydroxyproline may be substituted for
30 proline; 5-hydroxylysine may be substituted for lysine; 3-methylhistidine may be substituted for histidine; homoserine may be substituted for serine; and ornithine may be substituted for lysine. Polypeptides of the present invention also include any
35 polypeptide having one or more additions relative to

the sequence of a polypeptide whose sequence is shown herein, so long as the requisite activity is maintained.

5 Additional residues may also be added at either terminus for the purpose of providing a "linker" by which the polypeptides of this invention can be conveniently affixed to a label or solid matrix, or carrier. Preferably the linker residues do not form NANBV structural antigens.

10 Labels, solid matrices and carriers that can be used with the polypeptides of this invention are described herein below.

Amino acid residue linkers are usually at least one residue and can be 40 or more residues, more often
15 1 to 10 residues, but do not form NANBV epitopes. Typical amino acid residues used for linking are tyrosine, cysteine, lysine, glutamic and aspartic acid, or the like. In addition, a subject polypeptide can differ, unless otherwise specified, from the
20 natural sequence of the NANBV polyprotein by the sequence being modified by terminal-NH₂ acylation, e.g., acetylation, or thioglycolic acid amidation, by terminal-carboxlyamidation, e.g., with ammonia, methylamine, and the like.

25 When coupled to a carrier to form what is known in the art as a carrier-hapten conjugate, a polypeptide of the present invention is capable of inducing antibodies that immunoreact with NANBV. In view of the well established principle of immunologic
30 cross-reactivity, the present invention therefore contemplates antigenically related variants of the polypeptides described herein. An "antigenically related variant" is a subject polypeptide that is capable of inducing antibody molecules that

immunoreact with a polypeptide of this invention and with NANBV.

Any peptide of the present invention may be used in the form of a pharmaceutically acceptable salt.

5 Suitable acids which are capable of forming salts with the peptides of the present invention include inorganic acids such as hydrochloric acid, hydrobromic acid, perchloric acid, nitric acid, thiocyanic acid, sulfuric acid, phosphoric acetic acid, propionic acid, 10 glycolic acid, lactic acid, pyruvic acid, oxalic acid, malonic acid, succinic acid, maleic acid, fumaric acid, anthranilic acid, cinnamic acid, naphthalene sulfonic acid, sulfanilic acid or the like.

15 Suitable bases capable of forming salts with the peptides of the present invention include inorganic bases such as sodium hydroxide, ammonium hydroxide, potassium hydroxide and the like; and organic bases such as mono-, di- and tri-alkyl and aryl amines (e.g. triethylamine, diisopropyl amine, methyl amine, 20 dimethyl amine and the like) and optionally substituted ethanolamines (e.g. ethanolamine, diethanolamine and the like).

In general, the solid-phase synthesis methods contemplated comprise the sequential addition of one 25 or more amino acid residues or suitably protected amino acid residues to a growing peptide chain. Normally, either the amino or carboxyl group of the first amino acid residue is protected by a suitable, selectively removable protecting group. A different, 30 selectively removable protecting group is utilized for amino acids containing a reactive side group such as lysine.

Using a solid phase synthesis as exemplary, the protected or derivatized amino acid is attached to an 35 inert solid support through its unprotected carboxyl

or amino group. The protecting group of the amino or carboxyl group is then selectively removed and the next amino acid in the sequence having the complimentary (amino or carboxyl) group suitably protected is admixed and reacted under conditions suitable for forming the amide linkage with the residue already attached to the solid support. The protecting group of the amino or carboxyl group is then removed from this newly added amino acid residue, and the next amino acid (suitably protected) is then added, and so forth. After all the desired amino acids have been linked in the proper sequence, any remaining terminal and side group protecting groups (and solid support) are removed sequentially or concurrently, to afford the final polypeptide.

F. NANBV Structural Protein and Fusion Protein Compositions

In another embodiment, the present invention contemplates a composition containing a NANBV structural protein, preferably isolated, comprising an amino acid residue sequence that defines a NANBV structural antigen of this invention.

By isolated is meant that a NANBV structural protein of this invention is present in a composition as a major protein constituent, typically in amounts greater than 10% of the total protein in the composition, but preferably in amounts greater than 90% of the total protein in the composition.

A NANBV structural antigen, as used herein, is a structural protein coded by the genome of NANBV and has the properties of an antigen as defined herein, namely, to be able to immunoreact specifically with an antibody. NANBV structural proteins have been tentatively designated as capsid and envelope, and have been partially characterized as described herein

to contain the NANBV structural antigens capsid and envelope, respectively.

5 NANBV capsid antigen as described herein comprises an amino acid residue sequence that is immunologically related in sequence to the putative Hutch strain NANBV capsid antigen, whose sequence is contained in SEQ ID NO:1 from residue 1 to residue 120.

10 NANBV envelope antigen as described herein comprises an amino acid residue sequence that is immunologically related in sequence to the putative Hutch strain NANBV envelope antigen, a portion of whose sequence is contained in SEQ ID NO:1 from residue 121 to residue 326.

15 By "immunologically related" is meant that sufficient homology in amino acid sequence is present in the two protein sequences being compared that antibodies specific for one protein immunoreact (cross-react) with the other protein. Immunological
20 cross-reactivity can be measured by methods well known including the immunoassay methods described herein.

 As used herein, the phrase "recombinant protein" refers to a protein of at least 20 amino acid residues in length, and preferably at least 50
25 residues, that includes an amino acid residue sequence that corresponds, and preferably is identical, to a portion of the NANBV structural protein contained in SEQ ID NO:1.

 In preferred embodiments a NANBV structural
30 protein includes an amino acid residue sequence that is immunologically related to, and preferably is identical to, the sequence contained in SEQ ID NO:1 from residue 1 to residue 20, from residue 21 to residue 40, from residue 2 to residue 40, or from
35 residue 1 to residue 74. The NANBV structural protein

with the indicated sequence is particularly preferred for use in diagnostic methods and systems because the capsid antigens contained therein were demonstrated herein to be particularly useful in detecting acute NANBV infection. Related NANBV structural proteins include a sequence contained in SEQ ID NO:1 from residue 1 to residue 120, from residue 1 to residue 176, and from residue 1 to residue 326. Exemplary are the proteins described herein having a sequence contained in SEQ ID NO:2 from residue 1 to residue 315, in SEQ ID NO:3 from residue 1 to residue 252, in SEQ ID NO:4 from residue 1 to residue 252, or in SEQ ID NO:6 from residue 1 to residue 271.

In another embodiment a NANBV structural protein includes an amino acid residue sequence that is immunologically related to, and preferably is identical to, the sequence contained in SEQ ID NO:1 from residue 69 to residue 120. An exemplary NANBV structural protein has the sequence of the expressed protein coded for by the rDNA plasmid pGEX-3X-693:691.

Additional NANBV structural proteins containing NANBV envelope antigen are contemplated that include an amino acid residue sequence that is immunologically related to, and preferably is identical to, the sequence contained in SEQ ID NO:1 from residue 121 to residue 176. Exemplary are the proteins having a sequence of the expressed protein coded for by one of the rDNA plasmids pGEX-3X-15:17, pGEX-3X-15:18 and pGEX-2T-15:17.

In another embodiment, a NANBV structural protein is contemplated that comprises an amino acid residue sequence according to a polypeptide of this invention.

In preferred embodiments a NANBV structural protein is essentially free of both procaryotic antigens (i.e., host cell-specific antigens) and other

NANBV-related proteins. By "essentially free" is meant that the ratio of NANBV structural antigen to foreign antigen, such as procaryotic antigen, or other NANBV-related protein is at least 10:1, preferably is 100:1, and more preferably is 200:1.

The presence and amount of contaminating protein in a NANBV structural protein preparation can be determined by well known methods. Preferably, a sample of the composition is subjected to sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) to separate the NANBV structural protein from any protein contaminants present. The ratio of the amounts of the proteins present in the sample is then determined by densitometric soft laser scanning, as is well known in the art. See Guillian et al., Anal. Biochem., 129:277-287 (1983).

A NANBV structural protein can be prepared as an isolated protein, and more preferably essentially free of procaryotic antigens or NANBV non-structural antigens by the methods disclosed herein for producing NANBV structural proteins. Particularly preferred are methods which rely on the properties of a polypeptide region of a fusion protein, which region is present in the fusion protein to facilitate separation of the fusion protein from host cell proteins on the basis of affinity. Exemplary are the GST-containing fusion proteins whose amino acid residue sequences are contained in SEQ ID NOS:2, 3, 4 or 6 wherein the GST polypeptide region of each provides the fusion protein with a functional domain having an affinity to bind to the normal substrate for GST, namely glutathione. The purification of a fusion protein having a GST polypeptide region is described further herein.

In a related embodiment, the invention describes a polypeptide that defines a NANBV antigen. Thus, the

invention contemplates a polypeptide corresponding to a region of the NANBV polyprotein that defines an antigenic determinant of the virus that is useful as a NANBV antigen in serological assays or in an inoculum to induce anti-NANBV antisera, as described herein.

5 A polypeptide of this invention comprises a sequence of amino acids of about 7 to about 200 residues in length, preferably about 20 to 150 residues in length, that comprises an amino acid residue sequence defined by the nucleotide sequence of a polynucleotide of this invention.

A preferred polypeptide comprises an amino acid residue sequence that includes an amino acid residue sequence selected from the group of sequences consisting of residue 391 to residue 404 of SEQ ID NO:46, residue 246 to residue 256 of SEQ ID NO:46, residue 461 to residue 466 of SEQ ID NO:46, residue 473 to residue 482 of SEQ ID NO:46, and residue 2356 to residue 2379 of SEQ ID NO:46. In particularly preferred embodiments the polypeptide has an amino acid residue sequence that corresponds to the sequence shown in SEQ ID NO:46.

Insofar as a polypeptide is useful to distinguish Hutch isolates, the invention contemplates a polypeptide having a length from about 7 to about 200 amino acid residues and comprising an amino acid residue sequence that corresponds to a portion of the sequence of the Hutch c59 isolate of NANBV shown in SEQ ID NO:46. In this embodiment, the polypeptide has at least one amino acid residue difference in sequence when compared to the amino acid residue sequence of an isolate of NANBV selected from the group consisting of HCV-1, HCV-BK, HCV-J, HC-J1, HC-J4, HCV-JH and HCV-Hh.

Preferably, a polypeptide is immunoreactive with anti-Hutch strain NANBV antisera when measured in

standard serological immunoassays such as are described herein.

More preferably, a polypeptide contains at least one amino acid residue sequence difference in a
5 variable region of the NANBV viral genome-encoded polyprotein as defined herein, such as an amino acid residue sequence that is selected from the group of sequences consisting of the V variable region amino acid residue sequence (residue 386 to residue 411 of
10 SEQ ID NO:46), the V₁ variable region amino acid residue sequence (residue 246 to residue 275 of SEQ ID NO:46), the V₂ variable region amino acid residue sequence (residue 456 to residue 482 of SEQ ID NO:46), and the V₃ variable region amino acid residue sequence
15 (residue 2356 to residue 2379 of SEQ ID NO:46).

In another embodiment, a composition comprising an isolated fusion protein is also contemplated by the present invention that comprises a NANBV structural protein of this invention operatively linked at one or
20 both termini to another polypeptide by a peptide bond. The added polypeptide can be any polypeptide designed to increase the functional domains present on the fusion protein. The added functional domains are included to provide additional immunogenic epitopes,
25 to add mass to the fusion protein, to alter the solubility of the fusion protein, to provide a means for affinity-based isolation of the fusion protein, and the like. Exemplary added functional domains are the Thrombin or Factor Xa specific cleavage sites
30 provided when a subject fusion protein is produced in the vector pGEX-3X or pGEX-2T, respectively, as described herein. An additional exemplary domain is the GST-derived protein domain that allows rapid isolation using affinity chromatography to a solid
35 phase containing glutathione affixed thereto.

A Thrombin or Factor Xa cleavage site-containing domain is used herein, in one embodiment, to allow production of an NANBV structural protein free of the GST function domain. Exemplary is the protein
5 produced in Example 6 having an amino acid residue sequence contained in SEQ ID NO:2 from residue 226 to residue 315. The Factor Xa cleavage site-containing domain is also used in the commercially available fusion protein expression vector pMAL available from
10 New England Biolabs (Beverly, MA) described herein.

In a related embodiment a NANBV structural protein is produced by Thrombin cleavage of a protein produced using the pGEX-2T vector, such as a protein having an amino acid residue sequence contained in SEQ
15 ID NO:3 from residue 225 to residue 252, in SEQ ID NO:4 from residue 225 to residue 252, or in SEQ ID NO:6 from residue 225 to residue 271.

A fusion protein of the present invention includes an amino acid residue sequence corresponding
20 from its amino-terminus to its carboxy-terminus to the amino acid residue sequence contained in SEQ ID NO:1 from residue 1 to residue 20, from residue 21 to residue 40, from residue 2 to residue 40, from residue 1 to residue 74, from residue 69 to residue 120, from
25 residue 121 to residue 176, or from residue 121 to residue 326. A preferred fusion protein has a sequence corresponding to, and more preferably is identical to, the amino acid residue sequence in SEQ
ID NO:2 from residue 1 to residue 315, in SEQ ID NO:3
30 from residue 1 to residue 252, in SEQ ID NO:4 from residue 1 to residue 252, or in SEQ ID NO:6 from residue 1 to residue 271. Other preferred fusion proteins are defined by the amino acid residue sequence of the expressed protein coding sequence
35 present in the rDNA plasmids pGEX-3X-690:694, pGEX-3X-

690:691, pGEX-3X-693:691, pGEX-3X-15:17, pGEX-3X-15:18, pGEX-2T-15:17, pGEX-2T-CAP-A, pGEX-2T-CAP-B, and pGEX-2T-CAP-A-B.

5 The phrase "fusion protein", when used herein refers to an isolated protein as it was defined for a NANBV structural protein of this invention. Thus an isolated fusion protein is a composition having a fusion protein of this invention in amounts greater than 10 percent of the total protein in the composition, and preferably greater than 90 percent of the total protein in the composition.

10 A preferred fusion protein is a heterologous fusion protein, that is, a fusion protein that contains a polypeptide portion derived from a protein originating in a heterologous species of virus, organism, pathogen or animal, i.e., a non-NANBV protein. Preferably a heterologous fusion protein contains a non-NANBV polypeptide portion that is not immunologically related to a NANBV structural antigen of this invention.

20 In one embodiment, a fusion protein contains a functional domain that provides an immunogenic or antigenic epitope other than the NANBV structural antigen defined herein and is preferably derived from a separate pathogen, or from several pathogens. The functional domain is immunogenic where that domain is present to form a polyvalent vaccine or immunogen for the purpose of inducing antibodies immunoreactive with both NANBV structural protein and a second pathogen. 25 The functional domain is antigenic where that domain is present to form a polyvalent antigen for use in diagnostic systems and methods for detecting at least two species of antibodies.

30 Of particular interest in this embodiment are fusion proteins designed to include a functional

35

domain that is derived from other hepatitis-causing viruses, such as Hepatitis B virus, and Hepatitis A virus. These viruses have been well characterized to contain antigenic determinants and immunogenic determinants suitable for use in the fusion protein of this invention, and provide the advantage of multipurpose biochemical reagents in both diagnostic and vaccine applications. Additionally, the included functional domain can contain amino acid sequences from other pathogens, preferably those which may also infect individuals with NANBV hepatitis, such as HIV.

Preferred NANBV structural proteins or fusion proteins comprising a NANBV structural antigen of the present invention are in non-reduced form, i.e., are substantially free of sulfhydryl groups because of intramolecular Cys-Cys bonding.

In preferred compositions, the NANBV structural protein or fusion protein as described herein, is present, for example, in liquid compositions such as sterile suspensions or solutions, or as isotonic preparations containing suitable preservatives.

One such composition useful for inducing anti-NANBV structural protein antibodies in a mammal is referred to as a vaccine and contains a NANBV structural protein or fusion protein of this invention.

G. Vaccines

1. Introduction

The word "vaccine" in its various grammatical forms is used herein to describe a type of inoculum containing one or more NANBV structural antigens of this invention as an active ingredient in a pharmaceutically acceptable excipient that is used to induce production of antibodies in a mammal

immunoreactive with NANBV, and preferably induce active immunity in a host mammal against NANBV.

5 An inoculum comprises, as an active immunogenic ingredient, an immunologically effective amount of at least one NANBV structural protein, polypeptide or fusion protein of this invention, or a combination thereof.

10 Because an inoculum is typically designed to induce specific antibodies, it is preferred that an inoculum contains a NANBV structural protein comprised of only NANBV structural antigens and not other functional domains as described for a fusion protein. Thus a preferred inoculum contains a NANBV structural protein of this invention that includes an amino acid residue sequence contained in SEQ ID NO:1 from residue 1 to residue 20, from residue 21 to residue 40, from residue 2 to residue 40, from residue 1 to residue 74, from residue 69 to residue 120, from residue 121 to residue 176, or from residue 121 to residue 326.

15 20 Particularly preferred as an active ingredient in an inoculum is a NANBV structural protein having the amino acid residue sequence contained in SEQ ID NO:1 from residue 1 to residue 20, from residue 21 to residue 40, from residue 2 to residue 40, from residue 1 to residue 74, from residue 1 to residue 120, or contained in SEQ ID NO:2 from residue 226 to residue 315, contained in SEQ ID NO:3 from residue 225 to residue 252, contained in SEQ ID NO:4 from residue 225 to residue 252, or contained in SEQ ID NO:6 from residue 225 to residue 271.

25 30

A preferred inoculum comprises the entire E₁ domain and E₂/NS1 domain encoded by a DNA sequence spanning nucleotides 571 to 2197 in SEQ ID NO:46.

35 An inoculum can contain one or more polypeptides of this invention as an active ingredient. Such

inoculums are particularly useful to produce an antibody immunoreactive with NANBV because the polypeptide can be designed to define a small and therefore unique epitope of the NANBV polyprotein. Such antibodies are isolate-specific as defined herein.

Alternatively, a polyvalent inoculum is contemplated that comprises a fusion protein that has more than 1 immunogenic functional domains and is useful to induce classes of antibodies specific for different antigens; namely a first NANBV structural antigen as described herein, or correspondence regions from different strains of HCV and a further antigen present on a distinct pathogen. Preferred further antigens are derived from pathogens that are typically found in association with NANBV-infected patients, namely Hepatitis B Virus, Human Immunodeficiency Virus (HIV) and the like.

A related embodiment contemplates two immunogenic domains, each from a different region of HCV, such that a single inoculum induces antibodies specific for two regions of the HCV encoded polyprotein.

2. Preparation

The preparation of an inoculum that contains a protein or polypeptide as an active ingredient is well understood in the art. Typically, such inoculums are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid prior to injection may also be prepared. The preparation can also be emulsified.

The active immunogenic ingredient is dissolved, dispersed or admixed in an excipient that is pharmaceutically acceptable and compatible with the active ingredient as is well known. The phrases "suitable for human use" and "pharmaceutically

acceptable" (physiologically tolerable) refer to molecular entities and compositions that typically do not produce an allergic or similar untoward reaction, such as gastric upset, dizziness and the like, when administered to a human. Suitable excipients may take a wide variety of forms depending on the intended use and are, for example, aqueous solutions containing saline, phosphate buffered saline (PBS), dextrose, glycerol, ethanol, or the like and combinations thereof. In addition, if desired, the inoculum can contain minor amounts of auxiliary substances such as wetting or emulsifying agents, pH buffering agents, mineral oils, carriers or adjuvants which enhance the effectiveness of the inoculum. A preferred embodiment contains at least about 0.01% to about 99% of NANBV structural protein or fusion as an active ingredient, typically at a concentration of about 10 to 200 μ g of active ingredient per ml of excipient.

3. Carriers

An inoculum may comprise a polypeptide or NANBV structural protein of this invention linked to a carrier, or an antigenic carrier, to facilitate the production of an immune response in the immunized mammal.

One or more additional amino acid residues may be added to the amino- or carboxy-termini of the NANBV structural protein to assist in binding the protein to a carrier if not already present on the protein. Cysteine residues added at the amino- or carboxy-termini of the protein have been found to be particularly useful for forming polymers via disulfide bonds. However, other methods well known in the art for preparing conjugates can also be used. Exemplary additional linking procedures include the use of Michael addition reaction products, dialdehydes such

as glutaraldehyde, Klipstein et al., J. Infect. Dis.,
147:318-326 (1983) and the like, or the use of
carbodiimide technology as in the use of a water-
soluble carbodiimide to form amide links to the
5 carrier.

Useful carriers are well known in the art, and
are generally proteins themselves. Exemplary of such
carriers are keyhole limpet hemocyanin (KLH), edestin,
thyroglobulin, albumins such as bovine serum albumin
10 (BSA) or human serum albumin (HSA), red blood cells
such as sheep erythrocytes (SRBC), tetanus toxoid,
cholera toxoid as well as poly amino acids such as
poly (D-lysine: D-glutamic acid), and the like.

As is also well known in the art, it is often
15 beneficial to bind a NANBV structural protein to its
carrier by means of an intermediate, linking group.
As noted above, glutaraldehyde is one such linking
group. However, when cysteine is used, the
intermediate linking group is preferably an
20 m-maleimidobenzoic acid N-hydroxysuccinimide ester
(MBS).

Additionally, MBS may be first added to the
carrier by an ester-amide interchange reaction.
Thereafter, the addition can be followed by addition
25 of a blocked mercapto group such as thiolacetic acid
(CH₃COSH) across the maleimido-double bond. After
cleavage of the acyl blocking group, a disulfide bond
is formed between the deblocked linking group
mercaptan and the mercaptan of the cysteine residue of
30 the protein.

Antigenic carriers can be utilized to potentiate
or boost the immune response (immunopotential), or
to direct the type of immune response by use of the
inoculum in combination with the carrier. See, for
35 example, the teachings of Milich et al., in U.S.

Patent Nos. 4,599,231, 4,599,230 and 4,683,136, and the teachings of Thornton et al., in U.S. Patent Nos. 4,818,527 and 4,882,145.

Other means of immunopotential include the use of liposomes and immuno-stimulating complex (ISCOM) particles. The unique versatility of liposomes lies in their size adjustability, surface characteristics, lipid composition and ways in which they can accommodate antigens. Methods to form liposomes are known in the art. See, for example, Prescott, Ed., Methods in Cell Biology, Vol. XIV, Academic Press, NY (1976) p.33 et seq. In ISCOM particles, the cage-like matrix is composed of Quil A, extracted from the bark of a South American tree. A strong immune response is evoked by antigenic proteins or peptides attached by hydrophobic interaction with the matrix surface.

The choice of carrier is more dependent upon the ultimate use of the immunogen than upon the determinant portion of the immunogen, and is based upon criteria not particularly involved in the present invention. For example, if an inoculum is to be used in animals, a carrier that does not generate an untoward reaction in the particular animal should be selected.

4. Administration

An inoculum is conventionally administered parenterally, by injection, for example, either subcutaneously or intramuscularly. Additional formulations which are suitable for other modes of administration include suppositories and, in some cases, oral formulations. For suppositories, traditional binders and carriers may include, for example, polyalkylene glycols or triglycerides; such suppositories may be formed from mixtures containing the active ingredient in the range of 0.5% to 10%,

preferably 1-2%. Oral formulations include such normally employed excipients as, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose, magnesium carbonate and the like. The compositions take the form of solutions, suspensions, tablets, pills, capsules, sustained release formulations or powders and contain 10%-95% of active ingredient, preferably 25-70%.

10 A NANBV structural protein can be formulated into an inoculum as a neutral or salt form. Pharmaceutically acceptable salts, include the acid addition salts (formed with the free amino groups of the antigen) and which are formed with inorganic acids such as, for example, hydrochloric or phosphoric acids, or such organic acids as acetic, oxalic, tartaric, mandelic, and the like. Salts formed with the free carboxyl groups can also be derived from inorganic bases such as, for example, sodium, potassium, ammonium, calcium, or ferric hydroxides, and such organic bases as isopropylamine, trimethylamine, histidine, procaine, and the like.

25 The inoculum is administered in a manner compatible with the dosage formulation, and in such amount as will be immunogenic and effective to induce an immune response. The quantity of inoculum to be administered to achieve desired full protective immunity when used as a vaccine depends on the subject to be immunized, capacity of the subject's immune system to synthesize antibodies or induce cell-mediated response, and the degree of protection desired. Precise amounts of active ingredient required to be administered depend on the judgement of the practitioner and are peculiar to each individual, but generally a dosage suitable for a broad population

can be defined. Suitable dosage ranges are of the order of about ten micrograms (μg) to several milligrams (mg), preferably about 10-500 micrograms and more preferably about 100 micrograms active ingredient for each single immunization dose for a human adult. Suitable regimes for initial administration and booster shots are also variable, but are typified by an initial administration followed in two to six week intervals by a subsequent injection or other administration.

An inoculum can also include an adjuvant as part of the excipient. Adjuvants such as complete Freund's adjuvant (CFA), incomplete Freund's adjuvant (IFA) for use in laboratory mammals are well known in the art. Pharmaceutically acceptable adjuvants such as alum can also be used. An exemplary inoculum thus comprises one ml of phosphate buffered saline (PBS) containing about 50 to 200 μg NANBV structural protein or polypeptide adsorbed onto about 0.5 mg to about 2.5 mg of alum, or to 0.1% to 1% $\text{Al}(\text{OH})_3$. A preferred inoculum comprises 1 ml of PBS containing 100 μg NANBV structural protein adsorbed onto 2.5 mg of alum carrier.

After administration of the inoculum, the mammal or human receiving the inoculum is maintained for a time period sufficient for the immune system of the mammal to respond immunologically, typically on the order of 2 to 8 weeks, as is well known, by the production of antibodies immunoreactive with the immunogen.

H. Antibody Compositions

An antibody of the present invention is a composition containing antibody molecules that immunoreact with a NANBV structural antigen, with the Hutch isolate of NANBV, preferably the c59 isolate,

and with a NANBV structural protein, polypeptide or fusion protein of the present invention (anti-NANBV structural protein antibody molecules). A preferred antibody contains antibody molecules that immunoreact with an epitope present on a polypeptide having an amino acid residue sequence contained in SEQ ID NO:1 from residue 1 to residue 326, preferably that immunoreacts with a polypeptide having the sequence contained in SEQ ID NO:1 from residue 1 to residue 20, from residue 21 to residue 40, from residue 2 to residue 40, from residue 1 to residue 74, from residue 49 to residue 120, or from residue 121 to residue 326.

In addition, it is preferred that anti-NANBV structural protein antibody molecules do not immunoreact with the NANBV isolates HCV-1, HCV-BK, HCV-J, HC-J1, HC-J4, HCV-JH or HCV-Hh, or with the C-100-3 antigen described herein, and available in the commercial assay available from Ortho Diagnostics, Inc.

An antibody of the present invention is typically produced by immunizing a mammal with an inoculum containing Hutch c59 isolate or a NANBV structural protein or polypeptide of this invention and thereby induce in the mammal antibody molecules having immunospecificity for the NANBV structural antigens described herein. The antibody molecules are then collected from the mammal and isolated to the extent desired by well known techniques such as, for example, by using DEAE Sephadex to obtain the IgG fraction.

To enhance the specificity of the antibody, the antibodies may be purified by immunoaffinity chromatography using solid phase-affixed immunizing NANBV structural protein. The antibody is contacted with the solid phase-affixed NANBV structural protein for a period of time sufficient for the NANBV

structural protein to immunoreact with the antibody molecules to form a solid phase-affixed immunocomplex. The bound antibodies are separated from the complex by standard techniques.

5 To produce an antibody composition that does not immunoreact with the C-100-3 antigen or the NANBV isolates identified above, immunoadsorption methods are used to remove the undesirable immunospecificities. Immunoadsorption methods to
10 remove immunospecificities are generally well known and involve first contacting the antibody composition with a solid phase having affixed thereto one or more of the antigens or NANBV isolates to form an immunoadsorption admixture. Preferably, there is an
15 excess of antigen or NANBV in the solid phase in proportion to the antibodies in the composition having the undesirable immunospecificities in the immunoadsorption admixture.

 The immunoadsorption admixture is then maintained
20 under immunoreaction conditions and for a time period sufficient for an immunocomplex to form in the solid phase. Thereafter, the liquid and solid phases are separated, and the liquid phase is retained having the undesirable antibody molecules immunoadsorbed away
25 onto the solid phase.

 Particularly preferred is an antibody composition containing c59 isolate specific antisera, formed by immunization with Hutch c59 isolate, or preferably with a polypeptide of this invention selected as
30 defined herein to have an amino acid residue sequence unique to c59 and preferably derived from the V, V1, V2 or V3 variable regions of NANBV. Thereafter, the produced antibody composition is immunoadsorbed to remove antibodies immunoreactive with NANBV isolates
35 other than c59 as described herein.

The antibody so produced can be used, inter alia, in the diagnostic methods and systems of the present invention to detect NANBV structural antigens as described herein present in a body sample.

5 The word "inoculum" in its various grammatical forms is used herein to describe a composition containing a NANBV structural antigen of this invention as an active ingredient used for the preparation of antibodies immunoreactive with NANBV
10 structural antigens.

 The preparation and use of an inoculum for production of an antibody of this invention largely parallels the descriptions herein for a vaccine insofar as the vaccine is also designed to induce the
15 production of antibodies and is exemplary of the preparation and use of an inoculum. A key difference is that the inoculum is formulated for use on an animal rather than a human, as is well known.

 A preferred antibody is a monoclonal antibody and
20 can be used in the same manner as disclosed herein for antibodies of the present invention.

 A monoclonal antibody is typically composed of antibodies produced by clones of a single cell called a hybridoma that secretes (produces) but one kind of
25 antibody molecule. The hybridoma cell is formed by fusing an antibody-producing cell and a myeloma or other self-perpetuating cell line. The preparation of such antibodies were first described by Kohler and Milstein, Nature 256:495-497 (1975), which description
30 is incorporated by reference. The hybridoma supernates so prepared can be screened for immunoreactivity with a NANBV structural antigen such as the NANBV structural protein used in the inoculum to induce the antibody-producing cell. Other methods

of producing monoclonal antibodies, the hybridoma cell, and hybridoma cell cultures are also well known.

Also contemplated by this invention is the hybridoma cell, and cultures containing a hybridoma cell that produce a monoclonal antibody of this invention.

It should be understood that in addition to the aforementioned carrier ingredients the pharmaceutical formulation described herein can include, as appropriate, one or more additional carrier ingredients such as diluents, buffers, binders, surface active agents, thickness, lubricants, preservatives (including antioxidants) and the like, and substances included for the purpose of rendering the formulation isotonic with the blood of the intended recipient. Typically, a preservative such as merthiolate (at a 1:5000 dilution of a 1% solution) is added to eliminate the risk of microbial contamination, even if sterile techniques were employed in the manufacture of the inoculum.

I. Diagnostic Systems and Methods

1. Diagnostic Systems

The present invention contemplates a diagnostic system for assaying for the presence of anti-NANBV antibodies or NANBV structural antigens in a body sample according to the diagnostic methods described herein.

A diagnostic system in kit form includes, in an amount sufficient for at least one assay according to the methods described herein, a NANBV structural protein, polypeptide or fusion protein or a combination thereof of the present invention, or an anti-NANBV antibody composition of this invention, as a separately packaged reagent. Instructions for use of the packaged reagent are also typically included.

"Instructions for use" typically include a tangible expression describing the reagent concentration or at least one assay method parameter such as the relative amounts of reagent and sample to be admixed, maintenance time periods for reagent/
5 sample admixtures, temperature, buffer conditions and the like.

In preferred embodiments, a diagnostic system of the present invention further includes a label or
10 indicating means capable of signaling the formation of a complex containing a NANBV structural antigen, a recombinant protein or an anti-NANBV antibody.

As used herein, the terms "label" and "indicating means" in their various grammatical forms refer to
15 single atoms and molecules that are either directly or indirectly involved in the production of a detectable signal to indicate the presence of a complex. Any label or indicating means can be linked to or incorporated in a reagent species such as an antibody
20 or monoclonal antibody, or can be used separately, and those atoms or molecules can be used alone or in conjunction with additional reagents. Such labels are themselves well-known in clinical diagnostic chemistry and constitute a part of this invention only insofar
25 as they are utilized with otherwise novel proteins, methods and/or systems.

The label can be a fluorescent labeling agent that chemically binds to antibodies or antigens without denaturing them to form a fluorochrome (dye)
30 that is a useful immunofluorescent tracer. Suitable fluorescent labeling agents are fluorochromes such as fluorescein isocyanate (FIC), fluorescein isothiocyanate (FITC), 5-dimethylamine-1-naphthalenesulfonyl chloride (DANSC),
35 tetramethylrhodamine isothiocyanate (TRITC),

lissamine, rhodamine 8200 sulfonyl chloride (RB 200 SC), a chelate-lanthanide bound (e.g., Eu, Tb, Sm) and the like. A description of immunofluorescence analysis techniques is found in DeLuca,
5 "Immunofluorescence Analysis", in Antibody As a Tool, Marchalonis, et al., eds., John Wiley & Sons, Ltd., pp. 189-231 (1982), which is incorporated herein by reference.

10 In preferred embodiments, the label is an enzyme, such as horseradish peroxidase (HRP), glucose oxidase, alkaline phosphatase or the like. In such cases where the principal label is an enzyme such as HRP or glucose oxidase, additional reagents are required to visualize the fact that an antibody-antigen complex
15 (immunoreactant) has formed. Such additional reagents for HRP include hydrogen peroxide and an oxidation dye precursor such as diaminobenzidine. An additional reagent useful with HRP is 2,2'-azino-di-(3-ethyl-benzthiazoline-6-sulfonic acid) (ABTS).

20 Radioactive elements are also useful labeling agents and are used illustratively herein. An exemplary radiolabeling agent is a radioactive element that produces gamma ray emissions. Elements which themselves emit gamma rays, such as ^{124}I , ^{125}I , ^{128}I , ^{131}I
25 and ^{51}Cr represent one class of gamma ray emission-producing radioactive element indicating groups. Particularly preferred is ^{125}I . Another group of useful labeling means are those elements such as ^{11}C , ^{18}F , ^{15}O and ^{13}N which themselves emit positrons. The
30 positrons so emitted produce gamma rays upon encounters with electrons present in the animal's body. Also useful is a beta emitter, such as ^{111}In , ^3H , ^{35}S , ^{14}C , or ^{32}P .

35 Additional labels have been described in the art and are suitable for use in the diagnostic systems of

this invention. For example, the specific affinity found between pairs of molecules can be used, one as a label affixed to the specific binding agent and the other as a means to detect the presence of the label. Exemplary pairs are biotin:avidin, where biotin is the label, and peroxidase:anti-peroxidase (PAP), where peroxidase is the label.

The linking of labels, i.e., labeling of, polypeptides and proteins is well known in the art. For instance, antibody molecules produced by a hybridoma can be labeled by metabolic incorporation of radioisotope-containing amino acids provided as a component in the culture medium. See, for example, Galfre et al., Meth. Enzymol., 73:3-46 (1981). The techniques of protein conjugation or coupling through activated functional groups are particularly applicable. See, for example, Aurameas, et al., Scand. J. Immunol., Vol. 8 Suppl. 7:7-23 (1978), Rodwell et al., Biotech., 3:889-894 (1984), and U.S. Pat. No. 4,493,795.

The diagnostic systems can also include, preferably as a separate package, a specific binding agent. A "specific binding agent" is a molecular entity capable of selectively binding a reagent species, which in turn is capable of reacting with a product of the present invention but is not itself a protein expression product of the present invention. Exemplary specific binding agents are antibody molecules such as anti-human IgG or anti-human IgM, complement proteins or fragments thereof, protein A, and the like. Preferably the specific binding agent can bind the anti-NANBV antibody to be detected when the antibody is present as part of an immunocomplex.

In preferred embodiments the specific binding agent is labeled. However, when the diagnostic system

includes a specific binding agent that is not labeled, the agent is typically used as an amplifying means or reagent. In these embodiments, the labeled specific binding agent is capable of specifically binding the amplifying means when the amplifying means is bound to a reagent species-containing complex.

The diagnostic kits of the present invention can be used in an "ELISA" format to detect the presence or quantity of antibodies in a body fluid sample such as serum, plasma or saliva. "ELISA" refers to an enzyme-linked immunosorbent assay that employs an antibody or antigen bound to a solid phase and an enzyme-antigen or enzyme-antibody conjugate to detect and quantify the amount of an antigen or antibody present in a sample. A description of the ELISA technique is found in Chapter 22 of the 4th Edition of Basic and Clinical Immunology by D.P. Sites et al., published by Lange Medical Publications of Los Altos, CA in 1982 and in U.S. Patents No. 3,654,090; No. 3,850,752; and No. 4,016,043, which are all incorporated herein by reference.

Thus, in preferred embodiments, the NANBV structural protein, polypeptide, fusion protein or anti-NANBV antibody of the present invention can be affixed to a solid matrix to form a solid support that is separately packaged in the subject diagnostic systems.

The reagent is typically affixed to the solid matrix by adsorption from an aqueous medium although other modes of affixation, well known to those skilled in the art, can be used.

Useful solid matrices are well known in the art. Such materials include the cross-linked dextran available under the trademark SEPHADEX from Pharmacia Fine Chemicals (Piscataway, NJ); agarose; beads of

polystyrene about 1 micron to about 5 millimeters in diameter available from Abbott Laboratories of North Chicago, IL; polyvinyl chloride, polystyrene, cross-linked polyacrylamide, nitrocellulose- or nylon-based webs such as sheets, strips or paddles; or tubes, plates or the wells of a microtiter plate such as those made from polystyrene or polyvinylchloride.

The present invention also contemplates a diagnostic system for assaying the presence of NANBV nucleic acids in a body sample using hybridization of polynucleotides or oligonucleotides of this invention to NANBV nucleic acids according to the diagnostic methods described herein.

A diagnostic system for assaying for the presence of NANBV nucleic acids in kit form includes, in an amount sufficient for at least one assay, a polynucleotide of the present invention, as a separately packaged reagent. Instructions for use of the packaged reagent are also typically included.

In preferred embodiments, a diagnostic system of this embodiment further includes a label or indicating means capable of signaling the formation of a hybridization complex containing a NANBV nucleic acid.

The NANBV structural protein, polypeptide, fusion protein, anti-NANBV antibody, polynucleotides, labeled specific binding agent or amplifying reagent of any diagnostic system described herein can be provided in solution, as a liquid dispersion or as a substantially dry power, e.g., in lyophilized form. Where the indicating means is an enzyme, the enzyme's substrate can also be provided in a separate package of a system. A solid support such as the before-described microtiter plate and one or more buffers can also be included as separately packaged elements in this diagnostic assay system.

The packages discussed herein in relation to diagnostic systems are those customarily utilized in diagnostic systems. Such packages include glass and plastic (e.g., polyethylene, polypropylene and polycarbonate) bottles, vials, plastic and plastic-foil laminated envelopes and the like.

2. Diagnostic Methods

The present invention contemplates any diagnostic method that results in detecting anti-NANBV structural protein antibodies or NANBV structural antigens in a body sample using a NANBV structural protein, polypeptide, fusion protein or anti-NANBV structural antigen antibody of this invention as an immunochemical reagent to form an immunoreaction product whose amount relates, either directly or indirectly, to the amount of material to be detected in the sample. Those skilled in the art will understand that there are numerous well known clinical diagnostic chemistry procedures in which an immunochemical reagent of this invention can be used to form an immunoreaction product whose amount relates to the amount of specific antibody or antigen present in a body sample.

Various heterogenous and homogenous protocols, either competitive or noncompetitive, can be employed in performing an assay method of this invention. Thus, while exemplary methods are described herein, the invention is not so limited.

To detect the presence of anti-NANBV structural protein antibodies in a patient, a body sample, and preferably a body fluid sample such as blood, plasma, serum, urine or saliva from the patient, is contacted by admixture under biological assay conditions with a NANBV antigenic molecule of this invention such as a NANBV structural protein, and preferably with a

polypeptide or fusion protein of the present invention, to form an immunoreaction admixture. The admixture is then maintained for a period of time sufficient to allow the formation of a NANBV antigenic molecule-antibody molecule immunoreaction product (immunocomplex). The presence, and preferably the amount, of complex can then be detected as described herein. The presence of the complex is indicative of anti-NANBV antibodies in the sample.

10 In preferred embodiments the presence of the immunoreaction product formed between NANBV antigenic molecules and a patient's antibodies is detected by using a specific binding reagent as discussed herein. For example, the immunoreaction product is first
15 admixed with a labeled specific binding agent to form a labeling admixture. A labeled specific binding agent comprises a specific binding agent and a label as described herein. The labeling admixture is then maintained under conditions compatible with specific
20 binding and for a time period sufficient for any immunoreaction product present to bind with the labeled specific binding agent and form a labeled product. The presence, and preferably amount, of labeled product formed is then detected to indicate
25 the presence or amount of immunoreaction product.

30 In preferred embodiments the diagnostic methods of the present invention are practiced in a manner whereby the immunocomplex is formed and detected in a solid phase, as disclosed for the diagnostic systems herein.

Thus, in a preferred diagnostic method, the NANBV structural protein or polypeptide is affixed to a solid matrix to form the solid phase. It is further preferred that the specific binding agent is protein
35 A, or an anti-human Ig, such as IgG or IgM, that can

complex with the anti-NANBV structural protein antibodies immunocomplexed in the solid phase with the NANBV structural protein. Most preferred is the use of labeled specific binding agents where the label is a radioactive isotope, an enzyme, biotin or a fluorescence marker such as lanthanide as described for the diagnostic systems, or detailed by references shown below.

In this solid phase embodiment, it is particularly preferred to use a recombinant protein that contains the antigen defined by the amino acid residue sequence contained in SEQ ID NO:1 from residue 1 to residue 20, from residue 21 to residue 40, from residue 2 to residue 40, or from residue 1 to residue 74, as embodied in the fusion proteins as described in Example 7.

In another preferred diagnostic method, the NANBV antigenic molecule of the invention is affixed to solid matrix as described above, and dilutions of the biological sample are subjected to the immunocomplexing step by contacting dilutions of sample with the solid surface and removing non-bound materials. Due to the multivalence of antibodies present in biological samples from infected individuals (bivalent for IgG, pentavalent for IgM) subsequent addition of labeled NANBV structural protein, polypeptide or fusion protein of the invention to this admixture will become attached to the solid phase by the sample antibody serving as bridge between the solid phase NANBV antigenic molecules of the invention and the soluble, labeled molecules. The presence of label in the solid phase indicates the presence and preferably the amount of specific antibody in the sample. One skilled in the art can determine a range of dilutions and determine

therefrom a concentration of labeled antigen in the solid phase. The biological sample and the labeled NANBV antigenic molecules of the invention can be admixed prior to, or simultaneously with contacting the biological sample with the solid phase allowing the trimolecular complex to form at the solid phase by utilizing the bridging property of bivalent or multivalent specific antibody. As a particularly useful label, biotinylated NANBV antigenic molecules of the invention can be the labeled antigen, allowing the subsequent detection by addition of an enzyme-streptavidin, or an enzyme-avidin complex, followed by the appropriate substrate. Enzymes such as horse-radish peroxidase, alkaline phosphatase, β -galactosidase or urease are frequently used and these, and other, along with several appropriate substrates are commercially available. Preferred labels with a marker which allows direct detection of the formed complex include the use of a radioactive isotope, such as, eg., iodine, or a lanthanide chelate such as Europium.

In another embodiment designed to detect the presence of a NANBV structural antigen in a body sample from a patient, the sample (e.g. blood, plasma, serum, urine or saliva) is contacted by admixture under biological assay conditions with an anti-NANBV structural protein antibody of this invention, to form an immunoreaction admixture. The admixture is then maintained for a period of time sufficient to allow the formation of a antigen-antibody immunoreaction product containing NANBV structural antigens complexed with an antibody of this invention. The presence and preferably amount, of complex can then be determined, thereby indicating the presence of antigen in the body fluid sample.

In a preferred embodiment, the antibody is present in a solid phase. Still further preferred, the amount of immunocomplex formed is measured by a competition immunoassay format where the antigen in a patient's body fluid sample competes with a labeled recombinant antigen of this invention for binding to the solid phase antibody. The method comprises admixing a body fluid sample with (1) solid support having affixed thereto an antibody according to this invention and (2) a labeled NANBV antigenic molecule of this invention that immunoreacts with the solid phase antibody to form a competition immunoreaction admixture that has both a liquid phase and a solid phase. The admixture is then maintained for a time period sufficient to form a labeled NANBV antigenic molecule-containing immunoreaction product in the solid phase. Thereafter, the amount of label present in the solid phase is determined, thereby indicating the amount of NANBV structural antigen in the body fluid sample.

Enzyme immunoassay techniques, whether direct or competition assays using homogenous or heterogenous assay formats, have been extensively described in the art. Exemplary techniques can be found in Maggio, Enzyme Immunoassay, CRC Press, Cleveland, OH (1981); and Tijssen, "Practice and Theory of Enzyme Immunoassays", Elsevier, Amsterdam (1988).

Biological assay conditions are those that maintain the biological activity of the NANBV antigenic molecules and the anti-NANBV structural protein antibodies in the immunoreaction admixture. Those conditions include a temperature range of about 4°C to about 45°C, preferably about 37°C, a pH value range of about 5 to about 9, preferably about 7, and an ionic strength varying from that of distilled water

to that of about one molar sodium chloride, preferably about that of physiological saline. Methods for optimizing such conditions are well known in the art.

Also contemplated are immunological assays
5 capable of detecting the presence of immunoreaction product formation without the use of a label. Such methods employ a "detection means", which means are themselves well-known in clinical diagnostic chemistry and constitute a part of this invention only insofar
10 as they are utilized with otherwise novel polypeptides, methods and systems. Exemplary detection means include methods known as biosensors and include biosensing methods based on detecting changes in the reflectivity of a surface (surface
15 plasmon resonance), changes in the absorption of an evanescent wave by optical fibers or changes in the propagation of surface acoustical waves.

Another embodiment contemplates detection of the immunoreaction product employing time resolved
20 fluorometry (TR-FIA), where the label used is able to produce a signal detectable by TR-FIA. Typical labels suitable for TR-FIA are metal-complexing agents such as a lanthanide chelate formed by a lanthanide and an aromatic beta-diketone, the lanthanide being bound to
25 the antigen or antibody via an EDTA-analog so that a fluorescent lanthanide complex is formed.

The principle of time-resolved fluorescence is described by Soini et al, Clin. Chem., 25:353-361 (1979), and has been extensively applied to
30 immunoassay. See for example, Halonen et al., Current Topics in Microbiology and Immunology, 104: 133-146 (1985); Suonpaa et al., Clinica Chimica Acta, 145:341-348 (1985); Lovgren et al., Talanta, 31:909-916 (1984); U.S. Patent Nos. 4,374,120 and 4,569,790; and
35 published International Patent Application Nos. EPO

139 675 and W087/02708. A preferred lanthanide for use in TR-FIA is Europium.

Regents and systems for practicing the TR-FIA technology are available through commercial suppliers
5 (Pharmacia Diagnostics, Uppsala, Sweden).

Particularly preferred are the solid phase immunoassays described herein in Example 7, performed as a typical "Western Blot".

The present diagnostic methods may be practiced
10 in combination with other separate methods for detecting the appearance of anti-NANBV antibodies in species infected with NANBV. For example, a composition of this invention may be used together with commercially available C100-3 antigen (Ortho
15 Diagnostics, Inc., Raritan, N.J.) in assays to determine the presence of either or both antibody species immunoreactive with the two antigens.

The present invention also contemplates the use of nucleic acid hybridization methods to detect the
20 presence of NANBV nucleic acids in a body sample using a polynucleotide or DNA segment of this invention. The method generally comprises a) forming an aqueous hybridization admixture by admixing a body sample with a polynucleotide or oligonucleotide of this invention;
25 b) maintaining the aqueous hybridization admixture for a time period and under hybridizing conditions sufficient for any NANBV polynucleic acids present in the body sample to hybridize with the admixed polynucleotides or oligonucleotides to form a
30 hybridization product; and c) detecting the presence of any of the hybridization product formed and thereby the presence of NANBV polynucleic acids in the body sample.

The NANBV nucleic acid sequence to be detected is
35 referred to herein as the target nucleic acid

sequence. Target nucleic acid sequences to be hybridized in the present methods can be present in any nucleic acid-containing sample so long as the sample is in a form, with respect to purity and concentration, compatible with nucleic acid hybridization reaction. Isolation of nucleic acids to a degree suitable for hybridization is generally known and can be accomplished by a variety of means. For instance, nucleic acids can be isolated from a variety of nucleic acid-containing samples including body tissue, such as skin, muscle, hair, and the like, and body fluids such as blood, plasma, urine, amniotic fluids, cerebral spinal fluids, and the like. See, for example, Maniatis et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory (1982); and Ausubel et al., Current Protocols in Molecular Biology, John Wiley and Sons (1987).

The hybridization reaction mixture is maintained in the contemplated method under hybridizing conditions for a time period sufficient for the polynucleotide or oligonucleotide probe to hybridize to complementary nucleic acid sequences present in the sample to form a hybridization product, i.e., a complex containing probe and target nucleic acid.

The phrase "hybridizing conditions" and its grammatical equivalents, when used with a maintenance time period, indicates subjecting the hybridization reaction admixture, in the context of the concentrations of reactants and accompanying reagents in the admixture, to time, temperature and pH conditions sufficient to allow the polynucleotide or oligonucleotide probe to anneal with the target sequence, typically to form a nucleic acid duplex. Such time, temperature and pH conditions required to accomplish hybridization depend, as is well known in

the art, on the length of the polynucleotide or oligonucleotide probe to be hybridized, the degree of complementarity between the polynucleotide or oligonucleotide probe and the target, the guanidine and cytosine content of the polynucleotide or oligonucleotide, the stringency of hybridization desired, and the presence of salts or additional reagents in the hybridization reaction admixture as may affect the kinetics of hybridization. Methods for optimizing hybridization conditions for a given hybridization reaction admixture are well known in the art.

Typical hybridizing conditions include the use of solutions buffered to pH values between 4 and 9, and are carried out at temperatures from 18 degrees C (18°C) to 75°C, preferably about 37°C to about 65°C, more preferably about 54°C, and for time periods from 0.5 seconds to 24 hours, preferably 2 minutes.

Hybridization can be carried out in a homogeneous or heterogeneous format as is well known. The homogeneous hybridization reaction occurs entirely in solution, in which both the polynucleotide probe and the nucleic acid sequences to be hybridized (target) are present in soluble forms in solution. A heterogeneous reaction involves the use of a matrix that is insoluble in the reaction medium to which either the polynucleotide probe or target nucleic acid is bound. For instance, the body sample to be assayed can be affixed to a solid matrix and subjected to in situ hybridization.

In situ hybridization is typically performed on a body sample in the form of a slice or section of tissue usually having a thickness in the range of about 1 micron to about 100 microns, preferably about 1 micron to about 25 microns and more preferably about

1 micron to about 10 microns. Such sample can be prepared using a commercially available cryostat.

Alternatively, a heterogeneous format widely used is the Southern blot procedure in which genomic DNA is electrophoresed after restriction enzyme digestion, and the electrophoresed DNA fragments are first denatured and then transferred to an insoluble matrix. In the blot procedure, a polynucleotide or oligonucleotide probe is then hybridized to the immobilized genomic nucleic acids containing complementary nucleic acid (target) sequences.

Still further, a heterogeneous format widely used is a library screening procedure in which a multitude of colonies, typically plasmid-containing bacteria or lambda bacteriophage-containing bacteria, is plated, cultured and blotted to form a library of cloned nucleic acids on an insoluble matrix. The blotted library is then hybridized with a polynucleotide or oligonucleotide probe to identify the bacterial colony containing the nucleic acid fragments of interest.

Typical heterogeneous hybridization reactions include the use of glass slides, nitro-cellulose sheets, and the like as the solid matrix to which target-containing nucleic acid fragments are affixed.

Also preferred are the homogeneous hybridization reactions such as are conducted for a reverse transcription of isolated mRNA to form cDNA, dideoxy sequencing and other procedures using primer extension reactions in which polynucleotide or oligonucleotide hybridization is a first step. Particularly preferred is the homogeneous hybridization reaction in which a specific nucleic acid sequence is amplified via a polymerase chain reaction (PCR).

Where the nucleic acid containing a target sequence is in a double-stranded (ds) form, it is

preferred to first denature the dsDNA, as by heating or alkali treatment, prior to conducting the hybridization reaction. The denaturation of the dsDNA can be carried out prior to admixture with a
5 polynucleotide or oligonucleotide to be hybridized, or can be carried out after the admixture of the dsDNA with the polynucleotide or oligonucleotide. Where the polynucleotide or oligonucleotide itself is provided as a double-stranded molecule, it too can be denatured
10 prior to admixture in a hybridization reaction mixture, or can be denatured concurrently therewith the target-containing dsDNA.

The method for detecting a specific target nucleic acid sequence is carried out by first
15 conducting the before-described hybridization reaction to form a hybridization product, and then detecting the presence of the formed hybridization product, thereby detecting the presence of the specific nucleic acid sequence in a nucleic acid-containing sample.

20 A nucleic acid-containing sample can be a body tissue or body fluid, and can be prepared as described before for hybridization reaction admixtures.

The detection of a hybridization product formed in the hybridization reaction can be accomplished by a
25 variety of means. Although there are preferred embodiments disclosed herein for hybridization product detection, it is to be understood that other well known detection means readily apparent to one skilled in the art are suitable for use in the presently
30 contemplated process and associated diagnostic system.

In one approach for detecting the presence of a specific nucleic acid sequence, the polynucleotide or oligonucleotide probe includes a label or indicating
35 group that will render a hybridization product in which the probe is present detectable. Typically such

labels include radioactive atoms, chemically modified nucleotide bases, and the like.

Radioactive elements operatively linked to or present as part of a polynucleotide or oligonucleotide probe provide a useful means to facilitate the detection of a hybridization product. A typical radioactive element is one that produces beta ray emissions. Elements that emit beta rays, such as ^3H , ^{14}C , ^{32}P , and ^{35}S represent a class of beta ray emission-producing radioactive element labels. A radioactive polynucleotide or oligonucleotide probe is typically prepared by enzymatic incorporation of radioactively labeled nucleotides into a nucleic acid using DNA polymerase, and then the labeled nucleic acid is denatured to form a radiolabeled polynucleotide or oligonucleotide probe.

Alternatives to radioactively labeled polynucleotide or oligonucleotide probes are polynucleotides or oligonucleotides that are chemically modified to contain metal complexing agents, biotin-containing groups, fluorescent compounds, and the like.

One useful metal complexing agent is a lanthanide chelate formed by a lanthanide and an aromatic beta-diketone, the lanthanide being bound to the nucleic acid, polynucleotide or oligonucleotide via a chelate forming compound such as an EDTA-analogue so that a fluorescent lanthanide complex is formed. See U.S. Patents No. 4,374,120, and No. 4,569,790 and published Patent Applications No. EP0139675 and No. WO87/02708.

Biotin or acridine ester-labeled oligonucleotides and their use in polynucleotides have been described. See U.S. Patent No. 4,707,404, published Patent Application EP0212951 and European Patent No. 0087636.

Useful fluorescent marker compounds include fluorescein, rhodamine, Texas Red, NBD and the like.

5 A labeled nucleotide present in a hybridization product renders the hybridization product itself labeled and therefore distinguishable over other nucleic acids present in a sample to be assayed. Detecting the presence of the label in the hybridization product and thereby the presence of the hybridization product, typically involves separating
10 the hybridization product from any labeled polynucleotide or oligonucleotide probe that is not hybridized to a hybridization product.

Techniques for the separation of single- stranded polynucleotide or oligonucleotides, such as non-
15 hybridization labeled polynucleotide or oligonucleotide probe, from a hybridized product are well known, and typically involve the separation of single-stranded from non-single- stranded nucleic acids on the basis of their chemical properties. More
20 often separation techniques involve the use of a heterogeneous hybridization format in which the non-hybridized probe is separated, typically by washing, from the hybridization product that is bound to a solid matrix. Exemplary is the Southern blot
25 technique, in which the matrix is a nitrocellulose sheet and the label is ^{32}P . Southern, J. Mol. Biol., 98:503 (1975).

In another embodiment, the hybridization product detection step comprises detecting an amplified
30 nucleic acid product. An amplified nucleic acid product is the product of an amplification process well known in the art that is referred to as the polymerase chain reaction (PCR).

Methods and systems for amplifying a specific
35 nucleic acid sequence are described in U.S. Patents

No. 4,683,195 and No. 4,683,202, both to Mullis et al.; and the teachings in PCR Technology, Erlich, ed., Stockton Press (1989); Faloona et al., Methods in Enzymol., 155:335-50 (1987); and Polymerase Chain Reaction, Erlich et al., eds., Cold Spring Harbor Laboratories Press (1989).

Examples

The following examples are given for illustrative purposes only and do not in any way limit the scope of the invention.

Example 1. Production of Recombinant DNA Molecules

A. Isolation of NANBV Clones and Sequence Analysis

(1) Isolation of NANBV RNA and Preparation of cDNA

As a source for NANB virions, blood was collected from a chimpanzee infected with the Hutchinson (Hutch) strain exhibiting acute phase NANBH. Plasma was clarified by centrifugation and filtration. NANB virions were then isolated from the clarified plasma by immunoaffinity chromatography on a column of NANBV IgG (Hutch strain) coupled to protein G sepharose. NANBV RNA was eluted from the sepharose beads by soaking in guanidinium thiocyanate and the eluted RNA was then concentrated through a cesium chloride (CsCl) cushion. Sambrook et al., Molecular Cloning: A Laboratory Manual, Sambrook et al., eds. Second Edition, Cold Spring Harbor Laboratory Press, NY (1989).

The purified NANBV RNA in picogram amounts was used as a template in a primer extension reaction admixture containing random and oligo dT primers, dNTPs, and reverse transcriptase to form first strand

5 cDNAs. The resultant first strand cDNAs were used as
templates for synthesis of second strand cDNAs in a
reaction admixture containing DNA polymerase I and
RNase H to form double stranded (ds) cDNAs (Sambrook
10 et al., supra). The synthesized ds cDNAs were
amplified using an asymmetric synthetic primer-adaptor
system wherein sense and anti-sense primers were
annealed to each other and ligated to the ends of the
double stranded NANBV cDNAs with T4 ligase under
15 blunt-end conditions to form cDNA-adaptor molecules.
Polymerase chain reaction (PCR) amplification was
performed as described below by admixing the cDNA-
adaptor molecules with the same positive sense adaptor
primers, dNTPs and TAQ polymerase (Promega Biotec,
20 Madison, WI) to prepare amplified NANBV cDNAs. The
resultant amplified NANBV cDNA sequences were then
used as templates for subsequent amplification in a
PCR reaction with specific NANBV oligonucleotide
primers.

(2) Synthesis of Oligonucleotides for
Use in NANBV Cloning

Oligonucleotides were selected to correspond to
the 5' sequence of Hepatitis C which putatively
encodes the NANBV structural capsid and envelope
25 proteins (HCV1 sequence: Okamoto et al., Jap. J. Exp.
Med., 60:167-177, 1990). The selected
oligonucleotides were synthesized on a Pharmacia Gene
Assembler according to the manufacturer's instruction,
purified by polyacrylamide gel electrophoresis and
30 have nucleotide base sequences and consecutive SEQ ID
NOs beginning with 15 and ending with 23 as shown in
Table 1.

TABLE 1

SYNTHETIC OLIGONUCLEOTIDES

	Oligo- nucleotide Designation ^a	Putative NANBV Region	Oligonucleotide Sequence	SEQ ID NO
5	690 (+)	Capsid 1-21	ATGAGCACGATTCCCAAACCT	15
	693 (+)	Capsid 146-162	GAGGAAGACTTCCGAGC	16
	694 (-)	Capsid 208-224	GTCTTGCCCTCGGGCCG	17
	691 (-)	Capsid 340-359	ACCCAAATTGCGCGACCTACG	18
10	14 (+)	Envelope 356-374	TGGGTAAGGTCATCGATAC	19
	15 (+)	Envelope 361-377	AAGGTCATCGATACCCT	20
	18 (-)	Envelope 512-529	AGATAGAGAAAGAGCAAC	21
	16 (-)	Envelope 960-981	GGACCAGTTCATCATCATATAT	22
	17 (-)	Envelope 957-976	CAGTTCATCATCATATCCCA	23

15

- a The oligonucleotides are numerically defined and their polarity is indicated as (+) and (-) indicating the sequence corresponds to the sense and anti-sense coding strand, respectively. All sequences are listed in the 5' to 3' orientation.

20

(3) PCR Amplification of NANBV cDNA

PCR amplification was performed by admixing the primer-adapted amplified cDNA sequences prepared in Example 1A(1) with the synthetic oligonucleotides 690 and 694 as primer (primer pairs 690:694). The resulting PCR reaction admixture contained the primer-adapted amplified cDNA template, oligonucleotides 690 and 694, dNTPs, salts (KCl and MgCl₂) and TAQ polymerase. PCR amplification of the cDNA was conducted by maintaining the admixture at a 37°C annealing temperature for 30 cycles. Aliquots of samples from the first round of amplification were reamplified at a 55°C annealing temperature for 30 cycles under similar conditions.

25

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(4) Preparation of Vectors Containing
PCR Amplified ds DNA

Aliquots from the second round of PCR
amplification were subjected to electrophoresis on a
5 5% acrylamide gel. After separation of the PCR
reaction products, the region of the gel containing
DNA fragments corresponding to the expected 690:694
amplified product of approximately 224 bp was excised
and purified following standard electroelution
10 techniques (Sambrook et al., supra). The purified
fragments were kinased and cloned into the pUC18
plasmid cloning vector at the Sma I polylinker site to
form a plasmid containing the DNA segment 690:694
operatively linked to pUC18.

15 The resulting mixture containing pUC18 and a DNA
segment corresponding to the 690:694 sequence region
was then transformed into the E. coli strain JM83.
Plasmids containing inserts were identified as lac⁻
(white) colonies on X-gal medium containing
20 ampicillin. pUC18 plasmids which contained the
690:694 DNA segment were identified by restriction
enzyme analysis and subsequent electrophoresis on
agarose gels, and were designated pUC18 690:694 rDNA
molecules.

25 (5) Sequencing of Hepatitis Clones
that Encode the Putative Capsid
Protein

Two independent colonies believed to contain a
pUC18 vector having the NANBV Hutch strain 690:694 DNA
30 segment (pUC18 690:694) that codes for the amino
terminus of the putative capsid protein were amplified
and used to prepare plasmid DNA by CsCl density
gradient centrifugation by standard procedures
(Sambrook et al., supra). The plasmids were sequenced
35 using ³⁵S dideoxy procedures with pUC 18 specific
primers. The two plasmids were independently

sequenced on both DNA strands to assure the accuracy of the sequence. The resulting sequence information is presented as base 1 to base 224 of SEQ ID NO:1.

Plasmid pUC18 690:694 contains a NANBV DNA segment that is 224 bp in length and when compared to the HCJ1 prototype sequence reveals two nucleotide substitutions and one amino acid residue difference in the amino terminal region of the putative capsid protein.

10 (6) Preparation of NANBV Clones from the 5' End of the Genome

To obtain the sequence of the NANBV Hutch genome encoding the remainder of the capsid region (Okamoto et al., supra), the oligonucleotides 693 and 691 (described in Table 1) were used in PCR reactions. cDNA was prepared as described in Example 1A(1) to viral NANBV RNA from Hutch and used in PCR amplification as described in Example 1A(3) with the oligonucleotide pair 693:691. The resultant PCR amplified ds DNA was then cloned into pUC18 cloning vectors and screened for inserts as described in Example 1A(4) to form pUC 18 693:691. Clones were then sequenced with pUC18 specific primers as described in Example 1A(5).

25 Plasmid pUC18 693:691 contains a NANBV DNA segment that is 157 bp in length and spans nucleotide bases 203 to 360 of SEQ ID NO:1. The segment does not extend to the sequence of the 693 primer used for generating the fragment. The sequence of this
30 fragment reveals three nucleotide differences when compared to the known sequence of HCJ1 and does not have any corresponding amino acid changes to the HCJ1 sequence.

To obtain the sequence of the NANBV Hutch genome encoding the putative envelope region (Okamoto et al.,
35

supra), the oligonucleotide primers 14 through 18 (described in Table 1) were used in various combinations with NANBV Hutch RNA samples. As a source of NANBV RNA, a liver biopsy specimen from a chimpanzee inoculated with the Hutch strain at 4 weeks post-inoculation and exhibiting acute infection was used. The biopsied sample was first frozen and then ground. The resultant powder was then treated with guanidine isothiocyanate for the extraction of RNA. RNA was extracted from the guanidium-treated liver samples with phenol in the presence of SDS at 65°C. The liver samples were extracted a second time, and then extracted with chloroform. The extracted RNA was precipitated at -20°C with isopropanol and sodium acetate.

The purified liver-derived RNA was used as a template in primer extension reactions with the oligonucleotides 18 and 16 to generate NANBV specific-cDNAs. To prepare cDNA to the Hutch strain amino-terminal protein coding sequences, anti-sense oligonucleotides, 18 and 16, were annealed to liver-derived Hutch RNA in the presence of dNTPs and reverse transcriptase at 42°C to form primer extension products. The first round of PCR amplification of the two cDNAs was performed by admixing the primer extension reaction products with separate pairs of oligonucleotides 14:16 (16 primed cDNA) and 14:18 (18 primed cDNA) for 30 cycles at 55°C annealing temperature. The PCR reactions were performed on the above admixture as in 1A(3). Aliquots from the 14:16 and 14:18 amplifications were used as templates for the second round of amplification in which the oligonucleotide pairs 15:17 and 15:18, respectively, were used as primers.

PCR reaction products from each of the primer pair reactions were analyzed by electrophoresis on low melt agarose gels. Following separation, the regions of the gel containing DNA fragments corresponding to the expected 15:17 and 15:18 amplified products of approximately 617 bp and 168 bp, respectively, were excised and eluted from the gel slices at 65°C. The resultant eluted fragments were purified by phenol and chloroform extractions. To clone the 15:17 and 15:18 fragments, the purified fragments were separately treated with the Klenow fragment of DNA polymerase and kinase for subsequent subcloning into the SmaI site of the pBluescript plasmid vector (Stratagene Cloning Systems, La Jolla, CA). Transformed E. coli DH5 colonies were analyzed for plasmid insert by restriction enzyme analysis as described in Example 1A(4).

pBluescript plasmid containing 15:17 or 15:18 DNA segments were purified using large scale CsCl plasmid preparation protocols. The DNA segments present in the amplified and purified plasmids were each sequenced as described in Example 1A(5).

The sequence of the 15:17 DNA segment is contained in SEQ ID NO:1 from nucleotide 361 to 978. The sequence of the 15:18 DNA segment is also presented in SEQ ID NO:1 from nucleotide 361 to 529. These two clones overlap by 168 bp of the 15:18 DNA segment.

The sequence results indicate that the 15:17 DNA segment differs by 30 nucleotides when compared to the HCJ1 sequence (Okamoto et al., supra) and also differs by ten amino acid residues. The 15:18 DNA segment differs by seven nucleotides and by three amino acid residues when compared to HCJ1. In the overlap region, the two DNA segments differ at two nucleotide

bases, namely, bases 510 and 511, where DNA segment 15:18 contains a C in place of a T and an A in place of a G, respectively, which results in a change of a serine in place of a glycine amino acid residue, at residue 171 of SEQ ID NO:1. The reason for these differences is unknown and may be due to a PCR artifact.

B. Production of Recombinant DNA (rDNA) that Encodes a Fusion Protein

(1) Isolation of the 690:694 Fragment from the pUC 18 Clone and Introduction of the Fragment into the pGEX-3X Expression Vector

The pUC18 vector containing the 690:694 DNA segment was subjected to restriction enzyme digestion with Eco RI and Bam HI to release the DNA segment that includes a sequence contained in SEQ ID NO:1 from base 1 to base 224 from the pUC18 vector. The released DNA segment was subjected to acrylamide gel electrophoresis and the DNA segment containing the 224 bp NANBV insert plus portions of the pUC 18 polylinker was then excised and eluted from the gel as described in Example 1A(4). The eluted DNA segment was extracted with a mixture of phenol and chloroform, and precipitated.

The precipitated DNA segment was resuspended to a concentration of 25 µg/ml in water and treated with the Klenow fragment of DNA polymerase I and dNTP to fill in the staggered ends created by the restriction digestion. The resultant blunt-ended 690:694 segment was admixed with the bacterial expression vector, pGEX-3X, (available from Pharmacia Inc., Piscataway, NJ) which was linearized with the blunt end restriction enzyme Sma I. The admixed DNAs were then covalently linked (ligated) by maintaining the admixture overnight at 16°C in the presence of ligase

buffer and 5 units of T4 DNA ligase to form a plasmid of 690:694 DNA segment operatively linked to pGEX-3X.

(2) Selection and Verification of
Correctly Oriented Ligated Insert

5 The ligation mixture containing the pGEX-3X
vector and the 690:694 DNA segment was transformed
into host E. coli strain W3110. Plasmids containing
inserts were identified by selection of host bacteria
10 containing vector in Luria broth (LB) media containing
ampicillin. Bacterial cultures at stationary phase
were subjected to alkaline lysis protocols to form a
crude DNA preparation. The DNA was digested with the
restriction enzyme Xho I. The single Xho I site,
15 which cleaves within the 690:694 DNA segment between
nucleotide positions 173 to 178 of SEQ ID NO:1, but
not within the pGEX-3X vector, was used to screen for
vector containing the 690:694 DNA segment.

 Several 690:694 DNA segment-containing vectors
were amplified and the resultant amplified vector DNA
20 was purified by CsCl density gradient centrifugation.
The DNA was sequenced across the inserted DNA segment
ligation junctions by ³⁵S dideoxy methods with a
primer that hybridized to the pGEX-3X sequence at
nucleotide positions 614 to 633 contained in SEQ ID
25 NO:2. Vectors containing 690:694 DNA segment having
the correct coding sequence for in-frame translation
of a NANBV structural protein were thus identified and
selected to form pGEX-3X-690:694.

(3) Structure of the Fusion Protein

30 The pGEX-3X vector is constructed to allow for
inserts to be placed at the C terminus of Sj26, a
26-kDa glutathione S-transferase (GST; EC 2.5.1.18)
encoded by the parasitic helminth Schistosoma
japonicum. Insertion of the 690:694 NANBV fragment
35 in-frame behind Sj26 allows for the synthesis of the

Sj26-NANBV fusion polypeptide. The NANBV polypeptide can be cleaved from the GST carrier by digestion with the site-specific protease factor Xa (Smith et al., Gene, 67:31-40, 1988).

5 The nucleotide and predicted amino acid sequence of the pGEX-3X-690:694 fusion transcript from the GST sequence through the 690:694 insert is presented in SEQ ID NO:2. The resulting rDNA molecule, pGEX-3X-690:694, is predicted to encode a NANBV fusion
10 protein having the amino acid residue sequence contained in SEQ ID NO:2 from amino acid residue 1 to residue 315. The resulting protein product generated from the expression of the plasmid is referred to as both the GST:NANBV 690:694 fusion protein and the
15 CAP-N fusion protein.

C. Production of Recombinant DNAs (rDNAs)
 that Encode NANBV Capsid and Envelope
 Fusion Proteins

pGEX-3X-693:691: Plasmid pGEX-3X-693:691
20 was formed by first subjecting the plasmid pUC 18 693:691 prepared in Example 1A(6) to restriction enzyme digestion with Eco RI and Bam HI as performed in Example 1B(1). The resultant released DNA segment having a sequence contained in SEQ ID NO:1 from base
25 205 to base 360 was purified as performed in Example 1B(1). The purified DNA segment was admixed with and ligated to the pGEX-3X vector which was linearized by restriction enzyme digestion with Eco RI and Bam HI in the presence of T₄ ligase at 16°C to form the plasmid
30 pGEX-3X-693:691.

 A pGEX-3X plasmid containing a 693:691 DNA segment was identified by selection as performed in Example 1B(2) with the exception that crude DNA preparations were digested with Eco RI and Bam HI to
35 release the 693:691 insert. A pGEX-3X vector

containing a 693:691 DNA segment having the correct coding sequence for in-frame translation of a NANBV structural protein was identified by sequence analysis as performed in Example 1B(2) and selected to form pGEX-3X-693:691.

5 The resulting vector encodes a fusion protein (GST:NANBV 693:691) that is comprised of an amino-terminal polypeptide portion corresponding to residues 1 to 221 of GST as contained in SEQ ID NO:2, an intermediate polypeptide portion corresponding to residues 222 to 225 and defining a cleavage site for the protease Factor Xa, a linker protein corresponding to residues 226 to 230 consisting of the amino acid residue sequence (SEQ ID NO:25):

15 Gly Ile Pro Asn Ser
encoded by the nucleotide base sequence (SEQ ID NO:24):

GGG ATC CCC AAT TCA, respectively;
a carboxy-terminal polypeptide portion corresponding to residues 231 to 282 defining a NANBV capsid antigen having the amino acid residue sequence 69 to 120 in SEQ ID NO:1, and a carboxy-terminal linker portion corresponding to residues 283 to 287 consisting of the amino acid residue sequence (SEQ ID NO:27):

25 Asn Ser Ser END
encoded by the nucleotide base sequence (SEQ ID NO:26):

AAT TCA TCG TGA, respectively.

pGEX-3X-15:18: Plasmid pGEX-3X-15:18 was formed by first subjecting the plasmid Bluescript 15:18 prepared in Example 1A(6) to restriction enzyme digestion with Eco RV and Bam HI and the Bam HI cohesive termini were filled in as performed in Example 1B(1). The resultant released DNA segment having a sequence contained in SEQ ID NO:1 from base

361 to base 528 was purified as performed in Example 1B(1). The purified DNA segment was admixed with and ligated to the pGEX-3X vector which was linearized by restriction enzyme digestion with Sma I as performed in 1B(1) to form the plasmid pGEX-3X-15:18.

A pGEX-3X plasmid containing a 15:18 DNA segment was identified by selection as performed in Example 1B(2) and crude DNA preparations were cut with Eco RI and Bam HI to release the 15:18 inserts. A pGEX-3X vector containing a 15:18 DNA segment having the correct coding sequence for in-frame translation of a NANBV structural protein was identified as performed in Example 1B(2) and selected to form pGEX-3X-15:18.

The resulting vector encodes a fusion protein (GST:NANBV 15:18) that is comprised of an amino-terminal polypeptide portion corresponding to residues 1 to 221 of GST, an intermediate polypeptide portion corresponding to residues 222 to 225 and defining a cleavage site for the protease Factor Xa, a linker protein corresponding to residues 226 to 234 consisting of the amino acid residue sequence (SEQ ID NO:29):

Gly Ile Pro Ile Glu Phe Leu Gln Pro,
encoded by the nucleotide base sequence (SEQ ID NO:28):

GGG ATC CCC ATC GAA TTC CTG CAG CCC,
respectively; a carboxy-terminal polypeptide portion corresponding to residues 235 to 290 defining a NANBV envelope antigen having the amino acid residue sequence 121 to 176 in SEQ ID NO:1, and a carboxy-terminal linker portion corresponding to residues 291 to 298 consisting of a amino acid residue sequence (SEQ ID NO:31):

Trp Gly Ile Gly Asn Ser Ser END

encoded by the nucleotide base sequence (SEQ ID NO:30):

TGG GGG ATC GGG AAT TCA TCG TGA, respectively.

5 pGEX-3X-15:17: Plasmid pGEX-3X-15:17 was
formed by first subjecting the plasmid Bluescript
15:17 prepared in Example 1A(6) to restriction enzyme
digestion with Eco RI and Bam HI and the cohesive
termini were filled in as performed in Example 1B(1).
The resultant released DNA segment having a sequence
10 contained in SEQ ID NO:1 from base 361 to base 978 was
purified as performed in Example 1B(1). The purified
DNA segment was admixed with and ligated to the
pGEX-3X vector which was linearized by restriction
enzyme digestion with Sma I as performed in Example
15 1B(1) to form the plasmid pGEX-3X-15:17.

A pGEX-3X plasmid containing a 15:17 DNA segment
was identified by selection as performed in Example
1B(2) and DNA preparations were digested with Eco RI
and Bam HI as indicated above. pGEX-3X vector
20 containing a 15:17 DNA segment having the correct
coding sequence for in-frame translation of a NANBV
structural protein was identified as performed in
Example 1B(2) and selected to form pGEX-3X-15:17.

The resulting vector encodes a fusion protein
25 (GST:NANBV 15:17) that is comprised of an
amino-terminal polypeptide portion corresponding to
residues 1 to 221 of GST, an intermediate polypeptide
portion corresponding to residues 222 to 225 and
defining a cleavage site for the protease Factor Xa, a
30 linker protein corresponding to residues 226 to 233
consisting of the amino acid residue sequence (SEQ ID
NO:33):

Gly Ile Pro Asn Ser Cys Ser Pro
encoded by the nucleotide base sequence (SEQ ID
35 NO:32):

GGG ATC CCC AAT TCC TGC AGC CCT, respectively; a carboxy-terminal polypeptide portion corresponding to residues 234 to 439 defining a NANBV envelope antigen having the amino acid residue sequence 121 to 326 in SEQ ID NO:1, and a carboxy-terminal linker portion corresponding to residues 440 to 446 consisting of the amino acid residue sequence (SEQ ID NO:35):

Gly Ile Gly Asn Ser Ser END

encoded by the nucleotide base sequence (SEQ ID NO:34):

GGG ATC GGG AAT TCA TCG TGA, respectively.

pGEX-2T-15:17: Plasmid pGEX-2T-15:17 was formed by first subjecting the plasmid Bluescript 15:17 prepared in Example 1A(6) to restriction enzyme digestion with Eco RV and Bam HI and the Bam HI cohesive termini were filled in as performed in Example 1B(1). The resultant released DNA segment having a sequence contained in SEQ ID NO:1 from base 361 to base 978 was purified as performed in Example 1B(1). The purified DNA segment was admixed with and ligated to the pGEX-2T vector (Pharmacia, INC.) which was linearized by restriction enzyme digestion with Sma I as performed in Example 1B(1) to form the plasmid pGEX-2T-15:17.

A pGEX-2T plasmid containing a 15:17 DNA segment was identified by selection as performed in Example 1B(2) and by digestion of crude DNA preparations with Eco RI and Bam HI. A pGEX-2T vector containing a 15:17 DNA segment having the correct coding sequence for in-frame translation of a NANBV structural protein was identified as performed in Example 1B(2) and selected to form pGEX-2T-15:17.

The resulting vector encodes a fusion protein (GST:NANBV 15:17) that is comprised of an amino-terminal polypeptide portion corresponding to

residues 1 to 221 of GST, an intermediate polypeptide portion corresponding to residues 222 to 226 and defining a cleavage site for the protease Thrombin consisting of the amino acid residue sequence (SEQ ID NO:37):

Val Pro Arg Gly Ser

encoded by the nucleotide base sequence (SEQ ID NO:36):

GTT CCG CGT GGA TCC, respectively;

a linker protein corresponding to residues 227 to 233 consisting of an amino acid residue sequence (SEQ ID NO:39):

Pro Ser Asn Ser Cys Ser Pro

encoded by a nucleotide base sequence (SEQ ID NO:38):

CCA TCG AAT TCC TGC AGC CCT,

respectively; a carboxy-terminal polypeptide portion corresponding to residues 234 to 439 defining a NANBV envelope antigen, and a carboxy-terminal linker portion corresponding to residues 440 to 446 consisting of the amino acid residue sequence (SEQ ID NO:41):

Gly Ile His Arg Asp END

encoded by the nucleotide base sequence (SEQ ID NO:40):

GGA ATT CAT CGT GAC TGA, respectively.

pGEX-3X-690:691: To obtain a DNA segment corresponding to the NANBV Hutch sequence shown from SEQ ID NO:1 from base 1 to base 360, the oligonucleotides 690:691 are used in PCR reactions as performed in Example 1A(6). The resultant PCR amplified ds DNA is then cloned into pUC 18 cloning vectors as described in Example 1A(4) to form pUC18 690:691. Clones are then sequenced with pUC18 primers as described in Example 1A(5) to identify a plasmid containing the complete sequence. The resulting

identified plasmid is selected, is designated pUC18 690:691, and contains a NANBV DNA segment that is 361 bp in length and spans nucleotides 1 to 360 of SEQ ID NO:1.

5 Plasmid pGEX-3X-690:691 is formed by first
subjecting the plasmid pUC18 690:691 to restriction
enzyme digestion with Eco RI and Bam HI as performed
in Example 1B(1). The resultant released DNA segment
10 having a sequence contained in SEQ ID NO:1 from base 1
to base 360 with pUC18 polylinker sequence is purified
as performed in Example 1B(1). The purified DNA
segment is admixed with and ligated to the pGEX-3X
vector which is linearized by restriction enzyme
digestion with Sma I as performed in Example 1B(1) to
15 form the plasmid pGEX-3X-690:691.

 A pGEX-3X plasmid containing a 690:691 DNA
segment is identified by selection as performed in
Example 1B(2). pGEX-3X vector containing a 690:691
DNA segment having the correct coding sequence for in-
20 frame translation of a NANBV structural protein is
identified as performed in Example 1B(2) and selected
to form pGEX-3X-690:691.

 The resulting vector encodes a fusion protein
(GST:NANBV 690:691) that is comprised of an amino-
25 terminal polypeptide portion corresponding to residues
1 to 221 of GST, an intermediate polypeptide portion
corresponding to residues 222 to 225 and defining a
cleavage site for the protease Factor Xa, a linker
protein corresponding to residues 226 to 234
30 consisting of the amino acid residue sequence (SEQ ID
NO:43):

 Gly Ile Pro Asn Ser Ser Ser Val Pro
encoded by the nucleotide base sequence (SEQ ID
NO:42):

35 GGG ATC CCC AAT TCG AGC TCG GTA CCC

respectively; a carboxy-terminal polypeptide portion corresponding to residues 235 to 355 defining a NANBV capsid antigen, and a carboxy-terminal linker portion corresponding to residues 356 to 363 consisting of the amino acid residue sequence (SEQ ID NO:45):

Thr Gly Ile Gly Asn Ser Ser END

encoded by the nucleotide base sequence (SEQ ID NO:44):

ACG GGG ATC GGG AAT TCA TCG TGA, respectively.

pGEX-2T-CAP-A: Oligonucleotides 1-20(+) and 1-20(-) for constructing the vector pGEX-2T-CAP-A for expressing the CAP-A fusion protein were prepared as described in Example 1A(2) having nucleotide base sequences corresponding to SEQ ID NO:7 and SEQ ID NO:8, respectively.

Oligonucleotides 1-20 (+) and 1-20 (-) were admixed in equal amounts with the expression vector pGEX-2T (Pharmacia) that had been predigested with Eco RI and Bam HI and maintained under annealing conditions to allow hybridization of the complementary oligonucleotides and to allow the cohesive termini of the resulting double-stranded (ds) oligonucleotide product to hybridize with pGEX-2T at the Eco RI and Bam HI cohesive termini. After ligation the resulting plasmid designated pGEX-2T-CAP-A contains a single copy of the ds oligonucleotide product and a structural gene coding for a fusion protein designated CAP-A having an amino acid residue sequence shown in SEQ ID NO:3 from residue 1 to residue 252.

The pGEX-2T vector is similar to the pGEX-3X vector described above, except that the resulting fusion protein is cleavable by digestion with the site specific protease thrombin.

pGEX-2T-CAP-B: Oligonucleotides 21-40(+) and 21-40(-) for constructing the vector pGEX-2T-CAP-B for

expressing the CAP-B fusion protein were prepared as described in Example 1A(2) having nucleotide base sequences corresponding to SEQ ID NO:9 and SEQ ID NO:10, respectively.

5 Oligonucleotides 21-40 (+) and 21-40 (-) were admixed in equal amounts with the pGEX-2T expression vector that had been predigested with Eco RI and Bam HI and maintained under annealing conditions to allow hybridization of the complementary oligonucleotides
10 and to allow the cohesive termini of the resulting double-stranded oligonucleotide product to hybridize with pGEX-2T at the Eco RI and Bam HI cohesive termini. After ligation the resulting plasmid designated as pGEX-2T-CAP-B contains a single copy of
15 the ds oligonucleotide product and contains a structural gene coding for a fusion protein designated CAP-B having an amino acid residue sequence shown in SEQ ID NO:4 from residue 1 to residue 252.

pGEX-2T-CAP C: Oligonucleotides 41-60(+) and 41-
20 60(-) for constructing the vector pGEX-2T-CAP-C for expressing the CAP-C fusion protein were prepared as described in Example 1A(2) having nucleotide base sequences corresponding to SEQ ID NO:11 and SEQ ID NO:12, respectively.

25 Oligonucleotides 41-60 (+) and 41-60 (-) were admixed in equal amounts with the pGEX-2T expression vector that had been predigested with Eco RI and Bam HI and maintained under annealing conditions to allow hybridization of the complementary oligonucleotides
30 and to allow the cohesive termini of the resulting double-stranded oligonucleotide product to hybridize with pGEX-2T at the Eco RI and Bam HI cohesive termini. After ligation the resulting plasmid designated as pGEX-2T-CAP-C contains a single copy of
35 the double-stranded oligonucleotide product and

contains a structural gene coding for a fusion protein designated CAP-C having an amino acid residue sequence shown in SEQ ID NO:5 from residue 1 to residue 252.

pGEX-2T-CAP-A-B: Oligonucleotides for
5 constructing the vector pGEX-2T-CAP-A-B for expressing the CAP-A-B fusion protein were prepared as described in Example 1A(2) having nucleotide base sequences corresponding to SEQ ID NO:13 and SEQ ID NO:14, respectively.

10 Oligonucleotides according to SEQ ID NO:13 and SEQ ID NO:14 were admixed in equimolar amounts with the plasmid pGEX-3X-690:694 described in Example 1B(2). The admixture was combined with the reagents for a polymerase chain reaction (PCR) and the two
15 admixed oligonucleotides were used as primers on the admixed pGEX-3X-690:694 as template in a PCR reaction to form a PCR extension product consisting of a double-stranded nucleic acid molecule that encodes the amino acid residue sequence contained in SEQ ID NO:1
20 from residue 2 to 40 and also includes PCR-added restriction sites for Bam HI at the 5' terminus and Eco RI at the 3' terminus. The PCR extension product was then cleaved with the restriction enzymes Bam HI and Eco RI to produce cohesive termini on the PCR
25 extension product. The resulting product with cohesive termini was admixed in equal amounts with the pGEX-2T expression vector that had been predigested with Eco RI and Bam HI and maintained under annealing conditions to allow the cohesive termini of the
30 double-stranded PCR extension product to hybridize with pGEX-2T at the Eco RI and Bam HI cohesive termini. After ligation the resulting plasmid designated pGEX-2T-CAP-A-B contains a single copy of the double-stranded PCR extension product and contains
35 a structural gene coding for a fusion protein

designated CAP-A-B having an amino acid residue sequence shown in SEQ ID NO:6 from residue 1 to residue 271.

5 Example 2. Expression of the NANBV 690:694 Fusion Protein Using rDNA

10 The bacterial colonies which contain the pGEX-3X-690:694 plasmid in the correct orientation were selected to examine the properties of the fusion protein. Bacterial cultures of pGEX-3X-690:694 were grown to a stationary phase in the presence of
15 ampicillin (50 µg/ml final concentration) at 37°C. This culture was inoculated at a 1:50 dilution into fresh LB medium at 37°C in the presence of ampicillin and maintained at 37°C with agitation at 250 rpm until
20 the bacteria reached an optical density of 0.5 when measured using a spectrometer with a 550 nm wavelength light source detector. Isopropylthio-beta-D-galactoside (IPTG) was then admixed to the bacterial culture at a final concentration of 1 mM to initiate (induce) the synthesis of the fusion protein under the control of the tac promoter in the pGEX-3X vector.

25 Beginning at zero time and at one hour intervals thereafter for three hours following admixture with IPTG (i.e., the induction phase), the bacterial culture was maintained as above to allow expression of recombinant protein. During this maintenance phase, the optical density of the bacterial culture was
30 measured and 1 ml aliquots were removed for centrifugation. Each resultant cell pellet containing crude protein lysate was resuspended in Laemmli dye mix containing 1% beta-mercaptoethanol at a final volume of 50 µl for each 0.5 OD 550 unit. Samples

were boiled for 15 minutes and 10 μ l of each sample was electrophoresed on a 10% SDS-PAGE Laemmli gel.

Other GST:NANBV fusion proteins were also expressed in bacteria by transformation with the appropriate expression vector and induction as described above.

Example 3. Detection of Expressed Fusion Proteins

To visualize the IPTG-induced fusion proteins, the Laemmli gels were stained with Coomassie Blue and destained in acetic acid and methanol. Induced proteins from separate clones were examined and compared on the basis of the increase of a protein band in the predicted size range from time zero to time three hours post-IPTG treatment. Expression of fusion protein was observed in clones that exhibited an increase from zero time in the intensity of a protein band corresponding to the fusion protein.

The GST:NANBV fusion proteins CAP-A, CAP-B, and CAP-C, when analyzed on a 12.5% PAGE Laemmli gel as described in Example 2, exhibited an apparent molecular weight of about 30,000 daltons.

Example 4. Western Blot Analysis

Samples from IPTG inductions containing a GST:NANBV fusion protein of this invention were separated by gel electrophoresis and were transferred onto nitrocellulose for subsequent immunoblotting analysis. The nitrocellulose filter was admixed with antibody blocking buffer (20 mM sodium phosphate, pH 7.5, 0.5 M sodium chloride, 1% bovine serum albumin, and 0.05% Tween 40) for 3 to 12 hours at room temperature. Sera from humans or chimpanzees with NANB hepatitis believed to contain antibody immunoreactive with NANBV structural protein was

diluted 1:500 in the antibody blocking buffer and admixed with the nitrocellulose and maintained for 12 hours at room temperature to allow the formation of an immunoreaction product on the solid phase. The
5 nitrocellulose was then washed three times in excess volumes of antibody blocking buffer. The washes were followed by admixture of the nitrocellulose with 50 μ l of 125 I protein A (New England Nuclear, Boston, MA) at a 1:500 dilution in antibody blocking buffer for one
10 hour at room temperature to allow the labeled protein A to bind to any immunoreaction product present in the solid phase on the nitrocellulose. The nitrocellulose was then washed as described herein, dried and exposed to X-ray film for one to three hours at -70°C in order
15 to visualize the label and therefore any immunoreaction product on the nitrocellulose.

Results of the Western blot immunoassay are shown in Tables 2 through 7. Samples prepared using pGEX-3X vector that produces control GST were also prepared as
20 above and tested using the Western blot procedure as a control. The expressed GST protein was not detectable as measured by immunoreactivity using the sera shown to immunoreact with a fusion protein of this invention (e.g., GST:NANBV 690:694 fusion protein).

25
Example 5. Purification of Expressed GST:NANBV Fusion Proteins

Cultures of E. coli strain W3110 transformed with recombinant pGEX-3X-690:694 plasmids prepared in
30 Example 2 were cultured for 3 hours following IPTG induction treatment. The cells were then centrifuged to form a bacterial cell pellet, the cells were resuspended in 1/200 culture volume in lysis buffer (MTPBS: 150 mM NaCl, 16 mM Na_2HPO_4 , 4 mM NaH_2PO_4 , pH
35 7.3), and the cell suspension was lysed with a French

pressure cell. Triton X-100 was admixed to the cell lysate to produce a final concentration of 1%. The admixture was centrifuged at 50,000 X g for 30 minutes at 4°C. The resultant supernatant was collected and
5 admixed with 2 ml of 50% (w/v) glutathione agarose beads (Sigma, St. Louis, MO) preswollen in MTPBS. After maintaining the admixture for 5 minutes at 25°C to allow specific affinity binding between GST and glutathione in the solid phase, the beads were
10 collected by centrifugation at 1000 X g and washed in MTPBS three times.

The GST:NANBV 690:694 fusion protein was eluted from the washed glutathione beads by admixture and incubation of the glutathione beads with 2 ml of 50 mM
15 Tris HCl, pH 8.0, containing 5 mM reduced glutathione for 2 minutes at 25°C to form purified GST:NANBV 690:694 fusion protein.

The above affinity purification procedure produced greater than 95% pure fusion protein as
20 determined by SDS PAGE. That is, the purified protein was essentially free of procaryotic antigen and non-structural NANBV antigens as defined herein.

Alternatively, GST:NANBV 690:694 fusion protein was purified by anion exchange chromatography.
25 Cultures were prepared as described above and cell pellets were resuspended in 8M guanidine and maintained overnight at 4°C to solubilize the fusion protein. The cell suspension was then applied to an S-300 sepharose chromatography column and peak
30 fractions containing the GST:NANBV 690:694 fusion protein were collected, pooled, dialyzed in 4 M urea and subjected to anion exchange chromatography to form purified fusion protein.

Other GST:NANBV fusion proteins described herein
35 were also expressed in cultures of E.coli Strain W3110

as described above using the GST fusion protein vectors produced in Example 1 after their introduction by transformation into the E.coli host. After induction and lysis of the cultures, the GST fusion proteins were purified as described above using glutathione agarose affinity chromatography to yield greater than 95% pure fusion protein as determined by SDS-PAGE. Thus, CAP-A, CAP-B and CAP-C fusion proteins were all expressed and purified as above using the pGEX-2T-CAP-A vector, the pGEX-2T-CAP-B vector, or the pGEX-2T-CAP-C vector, respectively, and CAP-A-B fusion protein is expressed and purified using the PGEX-2T-CAP-A-B vector.

Example 6. Protease Cleavage of Purified GST:NANBV 690:694 Fusion Protein

Purified GST:NANBV 690:694 fusion protein prepared in Example 5 is subjected to treatment with activated Factor (Xa) (Sigma) to cleave the GST carrier from the NANBV 690:694 fusion protein (Smith et al., supra). Seven μ g of Factor X are activated prior to admixture with purified fusion proteins by admixture and maintenance with 75 nanograms (ng) activation enzyme, 8 mM Tris-HCl (pH 8.0), 70 mM NaCl and 8 mM CaCl_2 at 37°C for 5 minutes. Fifty μ g of purified fusion protein are then admixed with 500 ng activated human factor Xa in the elution buffer described in Example 5 containing 50 mM Tris HCl, 5 mM reduced glutathione, 100 mM NaCl, and 1 mM CaCl_2 , and maintained at 25°C for 30 minutes. The resulting cleavage reaction products are then absorbed on glutathione-agarose beads prepared in Example 5 to affinity bind and separate free GST from any cleaved NANBV structural antigen-containing protein. Thereafter the liquid phase is collected to form a

solution containing purified NANBV structural protein having an amino acid residue sequence contained in SEQ ID NO:2 from residue 226 to residue 315.

5 Example 7. Immunological Detection of Anti-NANBV Structural Protein Antibodies

10 NANBV Hutch strain virus was injected in chimpanzees and blood samples were collected at various weekly intervals post to inoculation (INOC) to analyze the immunological response to NANBV by five different diagnostic assays. Chimpanzees were categorized as either being in the acute or chronic phase of infection. The assays utilized in the evaluation of the immune response include: 1) alanine
15 aminotransferase (ALT) enzyme detection (Alter et al., JAMA, 246:630-634, 1981; and Aach et al., N. Engl. J. Med., 304:989-994, 1981); 2) histological evaluation for NANBV virions by electron microscopy (EM); 3)
20 detection of anti-HCV antibodies using the commercially available kit containing C100-3 antigen (Ortho Diagnostics, Inc.); 4) detection of anti-CAP-N antibodies by immunoblot analysis as described in Example 4 using the CAP-N fusion protein; and 5)
25 Detection of virus by PCR amplification as described in Example 1.

In Table 2, results are presented from ALT, EM, anti-HCV (anti-C100-3), anti-CAP-N, and PCR assays on sera from a chimpanzee with acute NANB Hepatitis.

TABLE 2

CHIMP 59 - ACUTE NANB HEPATITIS

	<u>WEEK POST INOC¹</u>	<u>ALT</u>	<u>EM</u>	<u>ANTI HCV</u>	<u>ANTI CAP-N²</u>	<u>PCR 690- 691</u>
5	8	26	++	-	-	-
	10	26	+	-	+	-
	12	107	+	-	+	-
	14	115	+	+	+	-
10	16	26	+	+	+	+
	18	17	ND	+	+	(+)
	20	11	ND	+	+	-

¹ Week after inoculation.

15 ² A plus (+) indicates immunoreaction was observed between admixed serum and the fusion protein, designated "CAP-N" because it corresponds to the amino terminal of the putative NANBV capsid protein, using the Western blot immunoassay described in Example 4.

20

25 The results in Table 2 show immunoreaction between fusion protein and anti-NANBV structural protein antibodies in the sera tested. Furthermore, seroconversion is detectable by the immunoassay using fusion protein containing capsid antigen at times earlier than when the same sera is assayed in the C100-3-based immunoassay.

30 In Table 3, results are presented from ALT, anti-HCV (anti-C100-3) and anti-CAP-N assays on sera collected from a human with definitive NANB Hepatitis.

TABLE 3

NYU - 169 - DEFINITIVE NANB HEPATITIS

	<u>Week Post Infect</u>	<u>ALT</u>	<u>Anti HCV</u>	<u>Anti CAP-N</u>
5	2	34	-	-
	6	8	-	-
	10	150	-	-
	12	118	-	-
10	14	183	-	+
	16	317	-	+
	19	213	-	+
	23	53	-	+

15

The results in Table 3 show that in the human series 169 seroconversion sera samples, the CAP-N antigen present in the fusion protein detects NANBV-specific antibodies as early as 14 weeks post inoculation, whereas the C100-3-based immunoassay does not detect any anti-NANBV antibody at the times studied.

20

In Table 4, results are presented from ALT, EM, anti-HCV, and anti-CAP-N assays on sera from a chimpanzee with a self limited infection presented.

25

100

TABLE 4

CHIMP 213 - SELF LIMITED INFECTION

	<u>Week Post Inoc</u>	<u>ALT</u>	<u>EM</u>	<u>Anti HCV</u>	<u>Anti CAP-N</u>
5	4	24	+	-	+
	6	34	+	-	+
	8	38	+	-	+
	13	28	ND	-	+
10	16	25	ND	-	+
	18	23	ND	+	+
	20	25	-	+	+

15 The results in Table 4 show that the CAP-N antigen detects anti-NANBV antibodies earlier than the C100-3 antigen when using sera sampled during the course of a self-limiting NANBV infection.

20 In Table 5, results are presented from ALT, anti-HCV and anti-CAP-N assays on sera from a chimpanzee that converted from an acute infection profile to a chronic one.

TABLE 5

CHIMP 10 - ACUTE/CHRONIC NANB HEPATITIS

	<u>Symptoms</u>	<u>Week Post Inoc</u>	<u>Peak ALT</u>	<u>Anti HCV</u>	<u>Anti CAP-N</u>
	acute	2	223	-	+
30	chronic	40	223	+	+
	chronic	42	223	+	+
	chronic	44	223	+	+
	chronic	51	223	+	-

35

The results in Table 5 indicate that the CAP-N antigen preferentially detects anti-NANBV antibodies in acute stages of NANBV infection.

5 In Table 6, results are presented from ALT, EM, anti-HCV (anti-C100-3) and anti-CAP-N assays on sera collected at various intervals from several chimpanzees with acute or chronic NANB Hepatitis.

TABLE 6

10

ADDITIONAL ACUTE SERA

	<u>Week Post Inoc</u>	<u>Week Post Alt Elev</u>	<u>Peak ALT</u>	<u>Anti HCV</u>	<u>Anti CAP-N</u>
	2	+1	73	-	+
15	14	+2	66	-	+
	6	+2	197	-	+
	11	+1	151	-	-
	8	+4	125	-	+
	15	+1	82	-	+
20	12	-4	73	ND	+

ADDITIONAL CHRONIC SERA

	156	+131	110	+	+
	156	-	89	+	+
25	160	-	89	+	+

30 The results in Table 6 indicate that the CAP-N antigen more often detected anti-NANBV antibodies in sera from acutely infected individuals than did the C100-3 antigen.

35 The results of Tables 2-6 show that the NANBV structural protein of the invention, in the form of a fusion protein containing CAP-N antigen and produced by the vector pGEX-3X-690:694, detects antibodies in

defined seraconversion series at times in an infected patient or chimpanzee earlier than detectable by present state of the art methods using the C100-3 antigen. In addition, the results show that CAP-N antigen is particularly useful to detect acute NANBV infection early in the infection.

Taken together, the results indicate that patients infected with NANBV contain circulating antibodies in their blood that are immunospecific for NANBV antigen designated herein as structural antigens, and particularly are shown to immunoreact with the putative capsid antigen defined by CAP-N. These antibodies are therefore referred to as anti-NANBV structural protein antibodies and are to be distinguished from the class of antibodies previously detected using the NANBV non-structural protein antigen C100-3.

In Table 7, comparative results are presented from anti-HCV capsid fusion protein assays according to the basic immunoblot assay described in Example 4 using various chimp and human sera on the following HCV capsid fusion proteins: CAP-N, CAP-A, CAP-B and CAP-C.

103

TABLE 7

	<u>SERA</u>	<u>TYPE^a</u>	<u>CAP-N^b</u>	<u>CAP-A^c</u>	<u>CAP-B^d</u>	<u>CAP-C^e</u>
	C18	Chimp 10 (A)	+++	+	+	-
	C10	Chimp 194(A)	+++	+++	+++	-
5	59-16	Chimp 59 (A)	+++	+	+++	ND
	59-12	Chimp 59 (A)	ND ^f	++	+++	-
	C9	Chimp 181(A)	+++	-	+++	-
	213-18	Chimp 213(A)	ND	+	+	-
<hr/>						
10	C2	Chimp 10 (C)	++	-	-	-
	C1	Chimp 10 (C)	+++	-	-	-
	C19	Chimp 10 (C)	+++	-	-	-
	C4	Chimp 68 (C)	+++	+++	+++	ND
<hr/>						
15	169-16	Human	ND	+++	+++	-
	169-23	Human	ND	+++	+++	-
	191-1	Human	+	+	+	ND
	191-2	Human	+	+	++	ND
	191-3	Human	+	+	+	ND
20	216-1	Human	-	+/-	+/-	ND
	216-2	Human	+	+	+	ND
	216-3	Human	+	+	+	ND

25 a The type of sera tested is indicated by the species (chimp or human), a chimp identification number if the sample is from a chimp, and a designation (in parenthesis) if the sera donor exhibits acute (A) or chronic (C) HCV infection at the time the sera was sampled.

30 b CAP-N indicates the GST:NANBV 690:694 fusion protein produced in Example 5 that includes HCV capsid protein residues 1 to 74.

35 c CAP-A indicates the GST:NANBV fusion protein produced in Example 5 that includes HCV capsid protein residues 1 to 20.

- d CAP-B indicates the GST:NANBV fusion protein produced in Example 5 that includes HCV capsid protein residues 21 to 40.
- e CAP-C indicates the GST:NANBV fusion protein produced in Example 5 that includes HCV capsid protein residues 41 to 60.
- f +, ++ and +++ indicate relative amounts of anti-HCV capsid antibody immunization product detected by the Western blot assay, where + indicates a weak band after overnight exposure of the x-ray film, ++ indicates a strong band after overnight exposure of the x-ray film, +++ indicates a strong band after 1 to 2 hours exposure of the X-ray film, and +/- or - indicates a faint or no band, respectively, after overnight exposure of the X-ray film
- g "ND" indicates not tested.

The results shown in Table 7 indicate that fusion proteins containing the CAP-A antigen or CAP-B antigen are immunoreactive with antibodies present in sera from HCV-infected humans or chimps. In addition, CAP-C antigen does not significantly immunoreact with sera from HCV infected humans or chimps.

Example 8. Characterization of NANBV Genomic RNA Sequence

A. Characterization of cDNA Clones and Primary Structure of NANBV

(1) Isolation of NANBV Viral RNA.

NANBV, also referred to as hepatitis C virus (HCV), was isolated from two tissue sources from a HCV-infected chimpanzee, number 59 (c59), that had been inoculated with the Hutch (H) strain of HCV (designated HCV-Hc59) as described in Example 1A(1). Chimpanzee liver was biopsied during the acute phase

of infection (4 weeks post-inoculation) and chimpanzee plasma was taken 13 weeks post-inoculation.

Extraction of nucleic acids from liver was performed as described by Ogata et al., Proc. Natl. Acad. Sci.,

5 USA, 88:3392-3396 (1991) and in Example 1A(6). HC virions were isolated from plasma having viral titers of $10^{5.5}$ to $10^{6.5}$ $\text{CID}_{50}/\text{ml}$. HCV RNA was purified from the plasma samples by either immunoaffinity chromatography as described in Example 1A(1) or by
10 isopropanol precipitation.

Briefly, 50 μl of plasma was diluted with an ice cold buffer solution containing 4.2 M guanidinium isothiocyanate, 0.5% sarcosyl and 0.025 M Tris-HCl at pH 8.0. The diluted plasma was then admixed with 50
15 μl of extraction buffer containing 100 mM Tris-HCl at pH 8.0, 10 mM EDTA and 1% SDS to form an extraction admixture. The admixture was vortexed and maintained at 5 minutes at 65°C to initiate extraction. Serum proteins were then removed from the admixture with
20 phenol/chloroform at 65°C followed by one extraction with chloroform alone. HCV RNA was then precipitated from the protein-free admixture by admixing two volumes of ice cold isopropanol and one-tenth volume of 3 M sodium acetate and maintaining the admixture
25 overnight at -20°C. After pelleting by centrifugation in an Eppendorf centrifuge at 1400 rpm for 30 minutes at 4°C, HCV RNA was washed once with 70% ethanol, vacuum dried and then resuspended in 9 μl RNase-free water. Purified HCV RNA samples were heated for 5
30 minutes at 65°C prior to cDNA synthesis performed as described below and in Example 1A(1).

(2) Cloning of HCV-Hc59 cDNA.

Five μg of purified liver or plasma derived HCV RNA was used per cDNA priming reaction. Specific
35 nucleotide primers derived from published HCV

sequences and spanning the entire reported genomic sequences were used to prime the reaction. See Okamoto et al., Japan. J. Exp. Med., 60:167-177 (1990); Kato et al., Proc. Natl. Acad. Sci., USA, 87:9524-9528 (1990); Han et al., Proc. Natl. Acad. Sci., USA, 88:1711-1715 (1991); and Houghton et al., European Patent Application Number 88310922.5 and Publication Number 318216. Selected target sequences were amplified using a PCR-based approach using a variety of nucleotide primers as described in Example 1A(3). The nucleotide sequences of the primers are listed in Table 8 below and have been identified by primer number and corresponding SEQ ID NOs.

15

TABLE 8

NUCLEOTIDE PRIMERS USED IN
CLONING HCV-HC59 CDNA

PRIMER (#)	SEQ ID NO.	NUCLEOTIDE SEQUENCE (5'-3')	POLARITY ^a
1	47	CAGCCCCCTGATGGGGGCGAC	+
22	48	ACTCGCAAGCACCCCTATCA	-
21	49	CTGTGAGGAACTACTGTCT	+
690	50	ATGAGCACGAATCCTCAAACCT	+
25	694	GTCCTGCCCTCGGGCC	-
	693	CGAGGAAGACTTCCGAGC	+
	691	ACCCAAATTGCGCGACCTAC	-
	15	TAAGGTCATCGATACCCT	+
	17	CAGTTCATCATCATATCCCA	-
30	18	AGATAGAGAAAGAGCAAC	-
	23	AGACTTCCGAGCGGTCGCAA	+
	717	GACCTGTGCGGGTCTGTC	+
	567	GGGTCGGCAGCTGGCTAGCCTCTCA	-
	801	TCCTGGCGGGCATAGCGT	+
35	8	CCCCAGCCCTGGTCAAAATCGGTAA	-
	568	TGAGAGGCTAGCCAGCTGCCGACCC	+

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	745	63	CTGTCGGTCGTTCCCACCA	-
	626	64	CCGCGAAGAGTGTGTGTGGT	+
	627	65	CAATGTTCTGGTGGAGGTG	-
	617	66	GCCATTAAGTGGGAGTACGTCGTTCTCC	+
5	652	67	CGAGGAAGGATACAAGACC	-
	628	68	TGCTTGTGGATGATGCTACT	+
	629	69	CACACGTGCAGTTGCGCT	-
	701	70	CTGCTGACCACTACACAG	+
	654	71	GACCAGAGTGGAAGCGCAA	+
10	653	72	TACCAGAGTCGGGTGTACAG	-
	500	73	CTAGGAGGCCCTTGTCTGC	-
	688	74	CTCGGGCCAGCCGATGGA	+
	633	75	GGGGACCTCATGGTTGTCT	-
	846	76	CCCGTGGAGTGGCTAAGG	+
15	831	77	CTCCTCGATGTTGGGATGG	-
	830	78	CAGAGCTTCCAGGTGGCTC	+
	795	79	CGGGCTCCGTCACCTGTG	+
	794	80	GTATTGCAGTCTATCACCGAG	-
	464	81	GGCTATAACGGCGACTTCGA	+
20	40	82	CGTTGAGTGCGGGAGACAG	-
	463	83	TCACCATTGAGACAATCACG	+
	788	84	GTAAGGAAGGTTCTCCCCACTC	-
	571	85	ATGCCCACCTTCTATCCCAGACAAAGC	+
	623	86	TGCATGTCATGATGTAT	-
25	841	87	GGACAAGACGACCCTGCC	-
	625	88	CGTATTGCCTGTCAACAGGC	+
	631	89	AGCGCCCAAAAGGCAGTAG	-
	842	90	CCTCTTCAACATATTGGGG	+
	843	91	CCAGGAACCGGAGCATGG	-
30	859	92	ACCAGTGGATAAGCTCGG	+
	904	93	CGTGGTGTAGGCATTAATG	-
	862	94	ATGTGGAGTGGGACCTTCC	+
	861	95	CTCTGCTGTTATATGGGAGG	-
	F4	96	GTTGACGTCCATGCTCACTG	+
35	A4	97	TTTCCACGTCTCCACTAGCG	-

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	849	98	GTGAGGACCACCGTCCGC	-
	F1	99	TTCCACCTCCAAAGTCCCCT	+
	2 ₁	100	AGAACTTGCAGTCTGTCAAATGTGA	-
	621	101	GGAAGAACAGAAACTGCCCCATCAATGCACTAAGC	+
5	2 ₀	102	TGACGCCGCTGCTTTAACCT	-
	2 ₂	103	TGCAAGCTTCCTCTACGGAT	-
	51	104	AGGTTAAAGCAGCGGCGTCA	+
	50	105	AGCTTCCCATCACGGCCAA	-
	502	106	GATGGCTTTGTACGACGTG	+
10	55	107	GCACCTGCGATAGCCGCAGT	-
	852	108	GTCCCTCACCGAGAGGCT	+
	853	109	GATTGGAGGTAGATCAAGTG	-
	4	110	TACGACTTGGAGCTCATAAC	+
	62	111	AGCAAGACACACTCCAGTCA	+
15	61	112	GCCTATTGGCCTGGAGTGGTTAGC	-

- (+) indicates sense strand
- (-) indicates anti-sense strand

20 Amplified sequences were subsequently isolated, rendered blunt-ended and inserted into a pUC or pBluescript (Stratagene) cloning vectors by standard procedures as described in Example 1A(4).

25 (3) Sequence Analysis of Cloned HCV-Hc59 cDNA

Clones were sequenced using the dideoxy chain termination method using a duPont automated sequencer Genesis 2000. In order to minimize sequencing errors due to PCR artifacts (misreading by Taq polymerase), three independent clones were isolated for each target sequence and were then sequenced. The resulting sequences were compared in order to derive the final consensus sequence representative of the HCV Hutch strain (HCV-H) genome. In some cases, several clones derived from independent studies encompassed the same

genomic domain. The sequences of these clones provided further confirmatory data.

(4) Characterization of cDNA Clones and Primary Structure of HCV-Hc59

5 Pairs of primers were selected as described above and in Example 1A(3) to amplify specific regions of the HCV-Hc59 genome to generate overlapping clones, the sequences of which would comprise the entire genome. The primer pairs used in specific PCR
10 reactions are listed in Table 9 below. The resultant forty cDNA clones generated from the selected primer pairs are listed numerically beginning with zero and ending with 39 in the same table and correspond to the putative map location shown in Figure 1. The deduced
15 size in base pairs of each isolated cDNA is also listed in Table 9.

TABLE 9
PCR DERIVED HCV-HC59 CLONES

20	<u>Clone #^a</u>	<u>Primer Pair^b</u>	<u>Insert Size (bp)^c</u>
	0	1:22	309
	1	21:22	268
	2	690:694	224
	3	693:691	216
25	4	15:18	170
	5	23:18	378
	6	15:17	618
	7	717:567	548
	8	801:8	346
30	9	568:745	205
	10	626:627	597
	11	617:652	173
	12	628:652	119
	13	628:629	390
35	14	701:652	314

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	15	654:653	106
	16	654:500	572
	17	688:633	590
	18	846:831	537
5	19	830:831	432
	20	795:794	313
	21	464:40	134
	22	463:788	347
	23	571:623	241
10	24	571:841	362
	25	625:631	482
	26	842:843	568
	27	859:904	320
	28	862:861	390
15	29	F4:A4	397
	30	F4:849	498
	31	F1:2 ₁	493
	32	621:2 ₁	132
	33	621:2 ₀	181
20	34	621:2 ₂	221
	35	51:50	360
	36	502:55	322
	37	852:853	625
	38	4:853	315
25	39	62:61	611

^a Relative location on HCV-Hc59 genome shown in Figure 1.

30 ^b Sense (+) and anti-sense (-) primer pairs having nucleotide sequences shown in Table 1 and in the Sequence Listings.

^c Deduced size in base pairs (bp) of the cloned insert produced by PCR using the indicated primer pair as described in Example 1A(3) and 8A(3).

35

Comparison of the sequences of three independently isolated cDNA clones from the same genomic domain revealed very few nucleotide differences indicating that the virus stock was homogeneous. The sequence of the complete HCV-H genome was deduced, representing 9416 nucleotides, which is similar in length to that of previously isolated HCV genomes, HCV-1, HCV-J, and HCV-BK. See, Kato et al., supra; Choo et al., Proc. Natl. Acad. Sci., USA, 88:2451-2455 (1991); and Takamizawa et al., J. Virol., 65:1105-1113 (1991). The sequence has a high GC content (58.8%), and contains one large open reading frame beginning at nucleotide base number 342 and ending at nucleotide base number 9374 (SEQ ID NO:46) corresponding to a protein of 3011 amino acid residues (SEQ ID NO:46). The deduced nucleotide sequences of HCV-Hc59 have been deposited in GenBank having the accession number M67463.

HCV-Hc59 sequences from the 5' and 3' end terminal non-coding (NC) domains, respectively encompassing 341 and 42 nucleotides, were identified. The first 12 nucleotides and the last 20 nucleotides (SEQ ID NO:46-see features) correspond to the nucleotide primers used in the amplification process and, thus are not confirmed as HCV-H sequences. However, 5' non-coding sequences of previously reported HCV genomes are extremely conserved (>98%), making it likely that the 5' end sequence of HCV-H reported here is very similar if not identical to the one indicated. However, due to greater divergence among HCV- 3' non-coding sequences, the HCV-Hc59 3' end sequence remains subject to confirmation. When an oligo (dT) primer was used for cDNA synthesis followed by PCR amplification using different combinations of primers, no viral sequences were obtained. This

result indicates that the viral genome lacks internal A-rich tracts at the 3' terminal end or a 3'-terminal poly (rA) sequence. Similarly, no sequences were amplified when A-rich primers complementary to the 3' end (U-rich) nucleotide sequence of the two reported Japanese isolates, HCV-J and HCV-BK, were used in the RT priming reaction, thus suggesting the absence of a U-rich terminal sequence in the genome of HCV-Hc59.

The large open reading frame of the HCV-Hc59 RNA genome is preceded by five AUG codons (cDNA = ATG - nucleotide base numbers 13, 32, 85, 96 and 214 as shown in SEQ ID NO:46) confirming the existence of hypothetical small open reading frames in the 5' NC region of HCV genomes. Several repeated sequences as shown in SEQ ID NO:46 listed as R₁ through R₅ in the features portion of the listing were identified in the 5' and the 3' NC regions, and in the C terminal of the putative NS5 domain. These sequences might correspond to important Cis acting elements involved in the regulation of viral replication.

The repeated sequences, R₂ and R₃, appear conserved among all HCV isolates. Although other repeated sequences have now been found in the terminal ends of HCV genomes, it is possible that sequences having a regulatory function would be sequences conserved among all HCV viruses, such as R₂ and R₃. The repeated sequence R₂ is particularly significant as it is represented by the highest copy number of four, is found within both the 5' and 3' terminal ends, and is localized upstream from a 3' terminal hairpin loop which may be involved in cyclization of viruses. Nothing is yet known about putative cyclization of HCV viruses. It is also possible that these very conserved self-complementary sequences may represent replicase recognition sites, possibly used

for both the plus and minus strands of the viral genome.

As described in previous reports for other HCV isolates, (Kato et al., Proc. Natl. Acad. Sci. USA, 87:9524-9528 (1990); Choo et al., Proc. Natl. Acad. Sci. USA, 88:2451-2455 (1991); and Takamizawa et al., J. Virol., 65:1105-1113 (1991)) the HCV-Hc59 genome or protein shares only limited similarity with other known viral sequences, except for three domains: (1) a few stretches of nucleotides in the 5' NC sequence are conserved with pestiviruses identical to those reported by Choo et al., supra, for the American prototype HCV-1 (SEQ ID NO:46), (2) blocks of amino acids found in the putative NS3 domain (nucleotide base numbers 3693 to 5198; SEQ ID NO:46) corresponding to putative NTP-binding helicase and trypsin-like serine proteases are conserved with flaviviruses and pestiviruses; and (3) the GDD consensus sequence conserved among all viral-encoded RNA-dependent RNA polymerases (amino acid residues 2737 to 2739; SEQ ID NO:46). In addition, a total of nineteen putative N-glycosylation sites were located, essentially clustered between amino acid residues 196 and 647 in a similar fashion to the organization observed for the envelope proteins of pestiviruses as described by Meyers et al., Virol., 171:555-567 (1989); and Collett et al., Virol., 162:167-180 (1988).

B. Comparison of Nucleotide and Protein Sequences of HCV-Hc59 and Heterologous HCV Isolates

A summary of the comparison between different genomic domains of HCV-Hc59 and the previously reported sequences for the American (HCV-1) or American-like (HC-J1) isolates, and for the Japanese isolates HC-J4, HCV-JH, HCV-J and HCV-BK is shown in

Table 10. Sequence comparison is limited with HC-J1, HC-J4 and HC-JH as the complete sequence of the genome of these isolates has not yet been reported. The hypothetical map assignments for HCV-encoded proteins deduced from sequence and hydrophobicity profile similarity between HCV genomes and flaviviruses and/or pestiviruses were used for making the comparison. The references for the compared sequences are listed at the bottom of Table 10. Based on sequence comparisons to related viruses, the HCV genome is believed to encode at least 8 domains as indicated in Table 10 : the structural domain consisting of the nucleocapsid (C) and two envelope (E1 and E2) proteins, and the non-structural region consisting of five proteins, NS2, NS3, NS4a, NS4b, and NS5. Domain designations are based on the organization of related HCV strains for comparative purposes, and do not necessarily reflect the domains of HCV-Hc59 because of the present state of the art in characterizing the domains of HCV-Hc59.

TABLE 10

HOMOLOGY OF NUCLEOTIDE AND DEDUCED AMINO ACID
SEQUENCE BETWEEN HCV-Hc59 AND HETEROLOGOUS ISOLATES

		<u>Isolate²</u>					
<u>Domain¹</u>		<u>HCV-1</u>	<u>HC-J1</u>	<u>HC-J4</u>	<u>HCV-JH</u>	<u>HCV-J</u>	<u>HCV-BK</u>
5	5'NC						
	-326-1						
	% bp ³	99.7	99.1	99.1	98.9	98.2	98.8
<hr/>							
	C						
10	1-570						
	bp	98.4	98.9	90.0	90.3	91.0	90.3
	aa	98.9	98.9	97.9	98.4	98.9	98.4
<hr/>							
	E1						
15	571-1140						
	bp	93.5	93.1	74.1	73.7	73.9	73.8
	aa	94.1	93.2	78.9	79.4	78.8	77.9
<hr/>							
	E2/NS1						
20	1141-2197						
	bp	93.6	91.7	67.7	65.4	73.5	71.2
	aa	92.9	88.7	70.7	65.6	79.3	80.4
<hr/>							
	NS2						
25	2198-3350						
	bp	93.8	--	--	--	72.4	72.7
	aa	95.1	--	--	--	80.0	78.2
<hr/>							
	NS3						
30	3351-4856						
	bp	95.4	--	--	--	80.1	78.9
	aa	97.2	--	--	--	92.2	92.6

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		<u>HCV-1</u>	<u>HC-J1</u>	<u>HC-J4</u>	<u>HCV-JH</u>	<u>HCV-J</u>	<u>HCV-BK</u>
	NS4a						
	4857-5596						
	bp	95.8	--	--	--	80.4	80.0
5	aa	95.5	--	--	--	87.0	86.2
	NS4b						
	5597-6049						
	bp	95.4	--	--	--	76.9	77.7
10	aa	96.7	--	--	--	84.8	85.4
	NS5						
	6050-9036						
	bp	95.9	--	--	--	78.3	79.3
15	aa	96.7	--	--	--	83.2	83.7
	3'NC						
	9037-9055						
	bp	83.3	--	--	--	73.6	63.1
20							

¹ Nucleotide position for C and E1 deduced from Weiner et al., Virology, 180:842-848 (1991) and for E₂ and NS2-NS5 from Takamizawa et al., J. Virology, 65:1105-1113 (1991);

² The nucleotide positions are calculated from the AUG initiation codon where A is base number 1.

³ The percentage of homology in base pairs (bp) and amino acid (aa) is listed.

30

The data indicate a very high degree of identity found in two genomic domains (5' NC and C) for all isolates despite geographical separation (90.0-98.9% nucleotide homology and 97.9 to 98.9% amino acid homology). A similar observation has been made in

35

flaviviruses that are members of the same sero-related subgroup by Brinton et al., Virology, 162:290-299 (1988), whereas members of different antigenic subgroups share only low levels of homology in that region. Two sets of repeated sequences found in the 5' NC domain, R₂ and R₃ (SEQ ID NO:46), are conserved among all reported isolates. Two copies of the repeated sequence R₁ are also conserved between the two American isolates HCV-Hc59 and HCV-1 but only one copy is found in both Japanese isolates HCV-J and HCV-BK. The 5' NC sequence of these genomes does not extend far enough to encompass the second copy. The nucleotide sequence reported for the other HCV isolates does not extend far enough into the 5' NC to allow for comparison.

Regions of moderate identity were found throughout the non-structural domains, where a clear separation between the two groups (American/Japanese) isolates could be seen. Whereas 93.8 to 95.9% nucleotide identity was observed when HCV-Hc59 was compared with the first group, only 72.7 to 80.0% identity was found with the second group (95.1 to 97.2% and 78.2-92.6% amino acid identity, respectively). One region, found in the putative NS5 (amino acid residue position 2356 to 2379 of SEQ ID NO:46) and called Region V₃ as shown in Table 11 below reflected even a more striking divergence between the two subgroups of HCV isolates. This region showed 100% identity between the two American isolates (data not shown) but only 12.5% with either Japanese strains. Although most of the changes appear to be conservative changes and might not therefore result in functional modification of the protein, it would be of interest to assess whether this genomic region is

immunologically active and if antigenic variation also exist between the two subgroups of HCV isolates.

Table 11¹

5

REGION V

(Residues 386 to 411 of

SEQ ID NO:46)

Isolates²

HCV-Hc59:

10

His Val Thr Gly Gly Asn Ala Gly Arg Thr Thr Ala
Gly Leu Val Gly Leu Leu Thr Pro Gly Ala Lys Gln
Asn Ile (SEQ ID NO:113)

HCV-1:

15

His Val Thr Gly Gly Ser Ala Gly His Thr Val Ser
Gly Phe Val Ser Leu Leu Ala Pro Gly Ala Lys Gln
Asn Val (SEQ ID NO:114)

HC-J1:

20

His Val Thr Gly Gly Gln Ala Ala Arg Ala Met Ser
Gly Leu Val Ser Leu Phe Thr Pro Gly Ala Lys Gln
Asn Ile (SEQ ID NO:115)

HCV-J:

25

His Val Thr Gly Gly Arg Val Ala Ser Ser Thr Gln
Ser Leu Val Ser Trp Leu Ser Gln Gly Pro Ser Gln
Lys Ile (SEQ ID NO:116)

HCV-BK:

30

His Val Thr Gly Gly Ala Gln Ala Lys Thr Thr Asn
Arg Leu Val Ser Met Phe Ala Ser Gly Pro Ser Gln
Lys Ile (SEQ ID NO:117)

119

HC-J4:

Tyr Thr Ser Gly Gly Ala Ala Ser His Thr Thr Ser
Thr Leu Ala Ser Leu Phe Ser Pro Gly Ala Ser Arg
Asn Ile (SEQ ID NO:118)

5

HCV-JH:

His Val Thr Gly Gly Val Gln Gly His Val Thr Ser
Thr Leu Thr Ser Leu Phe Arg Pro Gly Ala Ser Gln
Lys Ile (SEQ ID NO:119)

10

HCV-Hh-H77:

His Val Thr Gly Gly Ser Ala Gly Arg Thr Thr Ala
Gly Leu Val Gly Leu Leu Thr Pro Gly Ala Lys Gln
Asn Ile (SEQ ID NO:120)

15

HCV-Hh-H90:

His Val Thr Gly Gly Ser Ala Gly Arg Ser Val Leu
Gly Ile Ala Ser Phe Leu Thr Arg Gly Pro Lys Gln
Asn Ile (SEQ ID NO:121)

20

REGION V₁

(Residue 246 to 275 of
SEQ ID NO:46)

HCV-Hc59:

25 Val Ala Thr Arg Asp Gly Lys Leu Pro Thr Thr Gln
Leu Arg Arg His Ile Asp Leu Leu Val Gly Ser Ala
Thr Leu Cys Ser Ala Leu (SEQ ID NO:122)

HCV-1:

30 Val Ala Thr Arg Asp Gly Lys Leu Pro Ala Thr Gln
Leu Arg Arg His Ile Asp Leu Leu Val Gly Ser Ala
Thr Leu Cys Ser Ala Leu (SEQ ID NO:123)

120

HC-J1:

Val Ala Thr Arg Asp Gly Lys Leu Pro Ala Thr Gln
Leu Arg Arg His Ile Asp Leu Leu Val Gly Ser Ala
Thr Leu Cys Ser Ala Leu (SEQ ID NO:123)

5

HCV-J:

Leu Ala Ala Arg Asn Ser Ser Ile Pro Thr Thr Thr
Ile Arg Arg His Val Asp Leu Leu Val Gly Ala Ala
Ala Leu Cys Ser Ala Met (SEQ ID NO:124)

10

HCV-BK:

Leu Ala Ala Arg Asn Val Thr Ile Pro Thr Thr Thr
Ile Arg Arg His Val Asp Leu Leu Val Gly Ala Ala
Ala Phe Cys Ser Ala Met (SEQ ID NO:125)

15

HC-J4:

Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr
Ile Arg Arg His Val Asp Leu Leu Val Gly Ala Ala
Ala Phe Cys Ser Ala Met (SEQ ID NO:126)

20

HCV-JH:

Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr Thr
Leu Arg Arg His Val Asp Leu Leu Val Gly Thr Ala
Ala Phe Cys Ser Ala Met (SEQ ID NO:127)

25

HCV-Hh-H77:

Val Ala Thr Arg Asp Gly Lys Leu Pro Thr Thr Gln
Leu Arg Arg His Ile Asp Leu Leu Val Gly Ser Ala
Thr Leu Cys Ser Ala Leu (SEQ ID NO:122)

30

HCV-Hh-H90:

Val Ala Thr Arg Asp Gly Lys Leu Pro Thr Thr Gln
Leu Arg Arg His Ile Asp Leu Leu Val Gly Ser Ala
Thr Leu Cys Ser Ala Leu (SEQ ID NO:122)

35

121

REGION V₂

(Residue 456 to 482 of
SEQ ID NO:46)

5 HCV-Hc59:

Leu Ala Ser Cys Arg Arg Leu Thr Asp Phe Ala Gln
Gly Trp Gly Pro Ile Ser Tyr Ala Asn Gly Ser Gly
Leu Asp Gln (SEQ ID NO:128)

10 HCV-1:

Leu Ala Ser Cys Arg Pro Leu Thr Asp Phe Asp Gln
Gly Trp Gly Pro Ile Ser Tyr Ala Asn Gly Ser Gly
Pro Asp Gln (SEQ ID NO:129)

15 HC-J1:

Leu Ala Ser Cys Arg Arg Leu Thr Asp Phe Asp Gln
Gly Trp Gly Pro Ile Ser His Ala Asn Gly Ser Gly
Pro Asp Gln (SEQ ID NO:130)

20 HCV-J:

Met Ala Ser Cys Arg Pro Ile Asp Glu Phe Ala Gln
Gly Trp Gly Pro Ile Thr His Asp Met Pro Glu Ser
Ser Asp Gln (SEQ ID NO:131)

25 HCV-BK:

Met Ala Gln Cys Arg Thr Ile Asp Lys Phe Asp Gln
Gly Trp Gly Pro Ile Thr Tyr Ala Glu Ser Ser Arg
Ser Asp Gln (SEQ ID NO:132)

30 HC-J4:

Met Ala Ser Cys Arg Pro Ile Gln Trp Phe Ala Gln
Gly Trp Gly Pro Ile Thr Tyr Thr Glu Pro Asp Ser
Pro Asp Gln (SEQ ID NO:133)

35

122

HCV-Hh-H77:

Leu Ala Ser Cys Arg Arg Leu Thr Asp Phe Ala Gln
Gly Trp Gly Pro Ile Ser Tyr Ala Asn Gly Ser Gly
Leu Asp Glu (SEQ ID NO:128)

5

HCV-Hh-H90:

Leu Ala Ser Cys Arg Arg Leu Thr Asp Phe Asp Gln
Gly Trp Gly Pro Ile Ser Tyr Ala Asn Gly Ser Gly
Pro Asp Glu (SEQ ID NO:134)

10

REGION V₃
(Residue 2356 to 2379 of
SEQ ID NO:46)

HCV-Hc59:

15 Ser Thr Ser Gly Ile Thr Gly Asp Asn Thr Thr Thr
Ser Ser Glu Pro Ala Pro Ser Gly Cys Pro Pro Asp
(SEQ ID NO:135)

HCV-J:

20 Gly Ser Ser Ala Val Asp Ser Gly Thr Ala Thr Gly
Pro Pro Asp Gln Ala Ser Asp Asp Gly Asp Lys Gly
(SEQ ID NO:136)

HCV-BK:

25 Glu Ser Ser Ala Val Asp Ser Gly Thr Ala Thr Ala
Leu Pro Asp Gln Ala Ser Asp Asp Gly Asp Lys Gly
(SEQ ID NO:137)

1 Alignment of the deduced amino acid residue
30 sequence of Regions V, V₁, V₂, and V₃ of HCV-Hc59
with other American and Japanese isolates.

2 Isolates:

HCV-Hc59: American/Chimp 59; Inschauspe et al.,
Proc. Natl. Acad. Sci., USA, 1991;
35 GenBank Accession Number M67463;

- 5 HCV-1: American; Choo et al., Proc. Natl. Acad. Sci., USA, 88:2451-2455 (1991);
GenBank Accession Number M62321;
- HCV-1: 5' termini - Han et al., Proc. Natl. Acad. Sci., USA, 88:1711-1715 (1991);
Genbank Accession Number M58407;
- HCV-1: 3' termini - Han et al., supra; GenBank
Accession Number M58406;
- 10 HC-J1: American; Okamoto et al., Japan J. Exp. Med., 60:167-177 (1990);
- HCV-J: Japanese; Kato et al., Proc. Natl. Acad. Sci., USA, 87:9524-9528 (1990); Genbank
Accession Number D90208;
- 15 HCV-BK: Japanese; Takamizawa et al., J. Virol.,
65:1105-1113 (1991); Genbank Accession
Number M58335;
- HC-J4: Japanese; Okamoto et al., supra;
- HCV-JH: Japanese; Takeuchi et al., Nucl. Acids Res., 18:4626 (1990);
- 20 HCV-Hh-H77 and H90: American/human; Ogata et al.,
Proc. Natl. Acad. Sci., USA, 88:3392-3396
(1991).

25 Regions of greater divergence were found in the
putative envelope E1 (nucleotide base number 571 to
1140) and E2 (nucleotide base number 1141 to 2197 as
calculated from the AUG initiation codon), where 77.9
to 94.1% and 65.6 to 92.9% amino acid identity,
30 respectively, was observed between HCV-Hc59 and the
other isolates. In addition to the moderate and
hypervariable regions identified by Weiner et al.,
Viol., 180:842-848 (1991) in E1 and E2 (amino acid
residues 214 to 254 and 386 to 411, respectively) for
35 which protein heterogeneity between HCV-Hc59 and other

HCV isolates ranged from 70.7 to 97.6% for the moderate region (data not shown) and from 51.7 to 72.4% for Region V as shown in Table 11, two regions of high variability were identified. Both regions, Region V₁ and Region V₂ (amino acid residues 246 to 275 and 456-482, respectively) appeared very conserved among American or Japanese type HCV (96% identity) but showed striking heterogeneity when both groups were compared (55-58% protein identity, Table 11). In contrast to the observation made by Weiner et al., supra, who reported that approximately 50% of the amino acid changes observed in Region V between four American isolates and one Italian isolate are non-conservative changes, more than 85% of the changes observed in either Region V, V₁ or V₂ were found to consist of conservative changes. Although the function of these regions remain unknown, these data suggest that they are under immunological pressure and could be good candidates for targeting protective epitope domains that might be subtype specific in the case of Regions V₁ and V₂.

Thus, the genome of HCV-Hc59 shows an overall amino acid homology of 96% with the American prototype HCV-1 and 84.9% with both HCV-J and HCV-BK isolates. Three new regions of high variability were identified within E1, E2 and NS5 (Regions V₁, V₂ and V₃, respectively). In all three regions, sequence heterogeneity appears to be subgroup specific (i.e., American versus Japanese isolates), in particular for Region V₃ where up to 87.5% divergence was found between the two subgroups as shown in Tables 10 and 11. Sequence heterogeneity has been observed in the envelope/NS1 regions of flaviviruses (see, Meyers et al., Virology, 171:555-567 (1989); Collett et al., Virology, 165:191-199 (1988); and Hahn et al., Virology,

162:167-180 (1988) but not to the extent reported here for Regions V₁ and V₂, thus further suggesting that HCV structure is significantly divergent from this family of viruses. The fact that three of four
5 variable regions of the HCV genome are located in the putative envelope domains confirm that these domains are under great immunological pressure possibly associated with evolutionary-linked molecular divergence. A high rate of nucleotide change (28.2%)
10 in the putative E2/NS1 domain of HCV-H over an interval of thirteen years suggests significant evolution of the HCV genome in that domain. See Ogata et al., supra.

The cDNA sequence of the human prototype strain H
15 of HCV (9416 nucleotides) is the subject of this invention. To date, this is the second nucleotide sequence of a HCV genome determined for a prototype strain, as the two reported Japanese sequences HCV-J and HCV-BK have been derived from clones isolated from
20 a mixture of plasma therefore representing likely genomic sequences from multiple isolates. The data confirms that HCV exhibits a unique structure and organization more closely related to the pestiviruses than flaviviruses by the presence of stretches of
25 nucleotides highly conserved in the 5' NC domain, putative small open reading frames preceding the initial AUG codon, and putative NTP-binding helicases or trypsin-like serine proteases.

30 Description of SEQ ID NO:1-6 in the Sequence Listings

SEQ ID NO:1 contains the linear single-stranded nucleotide base sequence of a preferred DNA segment of the present invention that encodes portions of the structural proteins of the Hutch strain of NANBV. The
35 base sequences are shown conventionally from left to

right and in the direction of 5' terminus to 3' terminus using the single letter nucleotide base code (A=adenine, T=thymine, C=cytosine and G=guanine) with the position number of the first base residue in each row indicated to the left of the row showing the nucleotide base sequence.

The reading frame of the nucleotide sequence of SEQ ID NO:1 is indicated by placement of the deduced amino acid residue sequence of the protein for which it codes below the nucleotide sequence such that the triple letter code for each amino acid residue (Table of Correspondence) is located directly below the three bases (codon) coding for each residue. SEQ ID NO:1 also contains the linear amino acid residue sequence encoded by the nucleotide sequence of SEQ ID NO:1 and is shown conventionally from left to right and in the direction of amino terminus to carboxy terminus. The position number for every fifth amino acid residue is indicated below that amino acid residue sequence.

SEQ ID NO:2 contains the linear amino acid residue sequence of a preferred fusion protein designated CAP-N and is comprised of an amino-terminal polypeptide portion corresponding to residues 1 to 221 of glutathione-S-transferase, an intermediate polypeptide portion corresponding to residues 222 to 225 and defining a cleavage site for the protease Factor Xa, a linker portion corresponding to residues 226 to 234, a polypeptide portion corresponding to residues 235 to 308 defining a NANBV capsid antigen that has the amino acid residue sequence 1 to 74 in SEQ ID NO:1, and a carboxy-terminal linker portion corresponding to residues 309 to 315. SEQ ID NO:2 also contains the nucleotide base sequence of a linear single-stranded DNA segment that encodes the fusion protein described herein. The nomenclature and

presentation of sequence information is as described for SEQ ID NO:1.

5 SEQ ID NO:3 contains the linear amino acid residue sequence of a preferred fusion protein designated CAP-A and comprised of an amino-terminal polypeptide portion corresponding to residues 1 to 220 of glutathione-S-transferase, an intermediate polypeptide portion corresponding to residues 221 to 226 and defining a cleavage site for the protease
10 Thrombin, a polypeptide portion corresponding to residues 227 to 246 defining a portion of the NANBV capsid antigen that has the amino acid residue sequence 1 to 20 in SEQ ID NO:1, and a carboxy-terminal linker portion corresponding to residues 247
15 to 252. SEQ ID NO:3 also contains the nucleotide base sequence of a linear single-stranded DNA segment that encodes the fusion protein described therein. The nomenclature and presentation of sequence information is as described for SEQ ID NO:1.

20 SEQ ID NO:4 contains the linear amino acid residue sequence of a preferred fusion protein designated CAP-B and comprised of an amino-terminal polypeptide portion corresponding to residues 1 to 220 of glutathione-S-transferase, an intermediate
25 polypeptide portion corresponding to residues 221 to 226 and defining a cleavage site for the protease Thrombin, a polypeptide portion corresponding to residues 227 to 246 defining a portion of the NANBV capsid antigen that has the amino acid residue
30 sequence 21 to 40 in SEQ ID NO:1, and a carboxy-terminal linker portion corresponding to residues 247 to 252. SEQ ID NO:4 also contains the nucleotide base sequence of a linear single-stranded DNA segment that encodes the fusion protein described therein. The

nomenclature and presentation of sequence information is as described for SEQ ID NO:1.

5 SEQ ID NO:5 contains the linear amino acid residue sequence of a preferred fusion protein designated CAP-C and comprised of an amino-terminal polypeptide portion corresponding to residues 1 to 220 of glutathione-S-transferase, an intermediate polypeptide portion corresponding to residues 221 to 226 and defining a cleavage site for the protease
10 Thrombin, a polypeptide portion corresponding to residues 227 to 246 defining a portion of the NANBV capsid antigen that has the amino acid residue sequence 41 to 60 in SEQ ID NO:1, and a carboxy-terminal linker portion corresponding to residues 247
15 to 252. SEQ ID NO:5 also contains the nucleotide base sequence of a linear single-stranded DNA segment that encodes the fusion protein described therein. The nomenclature and presentation of sequence information is as described for SEQ ID NO:1.

20 SEQ ID NO:6 contains the linear amino acid residue sequence of a preferred fusion protein designated CAP-A-B and comprised of an amino-terminal polypeptide portion corresponding to residues 1 to 220 of glutathione-S-transferase, an intermediate
25 polypeptide portion corresponding to residues 221 to 226 and defining a cleavage site for the protease Thrombin, a polypeptide portion corresponding to residues 227 to 265 defining a portion of the NANBV capsid antigen that has the amino acid residue
30 sequence 2 to 40 in SEQ ID NO:1, and a carboxy-terminal linker portion corresponding to residues 266 to 271. SEQ ID NO:6 also contains the nucleotide base sequence of a linear single-stranded DNA segment that encodes the fusion protein described therein. The

nomenclature and presentation of sequence information is as described for SEQ ID NO:1.

5 The foregoing description and the examples are intended as illustrative and are not to be taken as limiting. Still other variations within the spirit and scope of this invention are possible and will readily present themselves to those skilled in the art. Other embodiments are within the following
10 claims.

130

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Zebedee, Suzanne
Inchauspe, Genevieve
Nasoff, Marc
Prince, Alfred
- (ii) TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS ANTIGEN,
DIAGNOSTIC METHODS AND VACCINES
- (iii) NUMBER OF SEQUENCES: 137
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: DRESSLER, GOLDSMITH, SHORE, SUTKER &
MILNAMOW, LTD.
 - (B) STREET: 180 N. Stetson, Suite 4700
 - (C) CITY: Chicago
 - (D) STATE: IL
 - (E) COUNTRY: USA
 - (F) ZIP: 60601
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/616369
 - (B) FILING DATE: 21-NOV-1990
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/573643
 - (B) FILING DATE: 25-AUG-1990
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Gamson, Edward P.
 - (B) REGISTRATION NUMBER: 29,381
 - (C) REFERENCE/DOCKET NUMBER: PHA0029P
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 312-616-5400
 - (B) TELEFAX: 312-616-5460

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 978 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..978
- (D) OTHER INFORMATION: /codon_start= 1
/product= "NANBV Structural Antigen"
/number= 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG	AGC	ACG	ATT	CCC	AAA	CCT	CAA	AGA	AAA	ACC	AAA	CGT	AAC	ACC	AAC	48
Met	Ser	Thr	Ile	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn	Thr	Asn	
1				5					10					15		
CGT	CGC	CCA	CAG	GAC	GTC	AAG	TTC	CCG	GGT	GGC	GGT	CAG	ATC	GTT	GGT	96
Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly	Gln	Ile	Val	Gly	
			20					25					30			
GGA	GTT	TAC	TTG	TTG	CCG	CGC	AGG	GGC	CCT	AGA	TTG	GGT	GTG	CGC	GCG	144
Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro	Arg	Leu	Gly	Val	Arg	Ala	
		35				40					45					
ACG	AGG	AAG	ACT	TCC	GAG	CGG	TCG	CAA	CCT	CGA	GGT	AGA	CGT	CAG	CCT	192
Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	
	50					55					60					
ATC	CCC	AAG	GCA	CGT	CGG	CCC	GAG	GGC	AGG	ACC	TGG	GCT	CAG	CCC	GGG	240
Ile	Pro	Lys	Ala	Arg	Arg	Pro	Glu	Gly	Arg	Thr	Trp	Ala	Gln	Pro	Gly	
65				70					75					80		
TAC	CCT	TGG	CCC	CTC	TAT	GGC	AAT	GAG	GGT	TGC	GGG	TGG	GCG	GGA	TGG	288
Tyr	Pro	Trp	Pro	Leu	Tyr	Gly	Asn	Glu	Gly	Cys	Gly	Trp	Ala	Gly	Trp	
			85			90								95		
CTC	CTG	TCT	CCC	CGT	GGC	TCT	CGG	CCT	AGC	TGG	GGC	CCC	ACA	GAC	CCC	336

132

Leu	Leu	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Ser	Trp	Gly	Pro	Thr	Asp	Pro	
			100					105					110			
CGG	CGT	AGG	TCG	CGC	AAT	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTT	ACG	TGC	384.
Arg	Arg	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys	
		115					120					125				
GGC	TTC	GCC	GAC	CTC	ATG	GGG	TAC	ATA	CCG	CTC	GTC	GGC	GCC	CCT	CTT	432 ³
Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu	
	130					135					140					
GGA	GGC	GCT	GCC	AGG	GCC	CTG	GCG	CAT	GGC	GTC	CGG	GTT	CTG	GAA	GAC	480
Gly	Gly	Ala	Ala	Arg	Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	
145					150					155					160	
GGC	GTG	AAC	TAT	GCA	ACA	GGG	AAC	CTT	CCT	GGT	TGC	TCT	TTC	TCT	ATC	528
Gly	Val	Asn	Tyr	Ala	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	
				165					170					175		
TTC	CTT	CTG	GCC	CTG	CTC	TCT	TGC	CTG	ACT	GTG	CCC	GCT	TCA	GCC	TAC	576
Phe	Leu	Leu	Ala	Leu	Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala	Tyr	
			180					185					190			
CAA	GTG	CGC	AAT	TCC	TCG	GGG	CTT	TAC	CAT	GTC	ACC	AAT	GAT	TGC	CCT	624
Gln	Val	Arg	Asn	Ser	Ser	Gly	Leu	Tyr	His	Val	Thr	Asn	Asp	Cys	Pro	
		195					200					205				
AAC	TCG	AGT	GTT	GTG	TAC	GAG	GCG	GCC	GAT	GCC	ATC	CTG	CAC	ACT	CCG	672
Asn	Ser	Ser	Val	Val	Tyr	Glu	Ala	Ala	Asp	Ala	Ile	Leu	His	Thr	Pro	
	210					215					220					
GGG	TGT	GTC	CCT	TGC	GTT	CGC	GAG	GGT	AAC	GCC	TCG	AGG	TGT	TGG	GTG	720
Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Gly	Asn	Ala	Ser	Arg	Cys	Trp	Val	
225					230					235					240	
GCG	GTG	ACC	CCC	ACG	GTG	GCC	ACC	AGG	GAC	GGC	AAA	CTT	CCC	ACA	ACG	768
Ala	Val	Thr	Pro	Thr	Val	Ala	Thr	Arg	Asp	Gly	Lys	Leu	Pro	Thr	Thr	
				245					250					255		
CAG	CTT	CGA	CGT	CAT	ATC	GAT	CTG	CTT	GTC	GGG	AGC	GCC	ACC	CTC	TGC	816
Gln	Leu	Arg	Arg	His	Ile	Asp	Leu	Leu	Val	Gly	Ser	Ala	Thr	Leu	Cys	
			260					265					270			
TCG	GCC	CTC	TAC	GTG	GGG	GAC	CTG	TGC	GGG	TCT	GTC	TTT	CTC	GTT	GGT	864
Ser	Ala	Leu	Tyr	Val	Gly	Asp	Leu	Cys	Gly	Ser	Val	Phe	Leu	Val	Gly	
		275					280					285				
CAA	CTG	TTT	ACC	TTC	TCT	CCC	AGG	CGC	CAC	TGG	ACG	ACG	CAA	GAC	TGC	912 ⁸
Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg	Arg	His	Trp	Thr	Thr	Gln	Asp	Cys	
	290					295					300					
AAT	TGT	TCT	ATC	TAT	CCC	GGC	CAT	ATA	ACG	GGT	CAT	CGC	ATG	GCA	TGG	960

133

Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met Ala Trp
 305 310 315 320

GAT ATG ATG ATG AAC TGG
 Asp Met Met Met Asn Trp
 325

978

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 948 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..945

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATG TCC CCT ATA CTA GGT TAT TGG AAA ATT AAG GGC CTT GTG CAA CCC	48
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro	
1 5 10 15	
ACT CGA CTT CTT TTG GAA TAT CTT GAA GAA AAA TAT GAA GAG CAT TTG	96
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu	
20 25 30	
TAT GAG CGC GAT GAA GGT GAT AAA TGG CGA AAC AAA AAG TTT GAA TTG	144
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu	
35 40 45	
GGT TTG GAG TTT CCC AAT CTT CCT TAT TAT ATT GAT GGT GAT GTT AAA	192
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys	
50 55 60	
TTA ACA CAG TCT ATG GCC ATC ATA CGT TAT ATA GCT GAC AAG CAC AAC	240
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn	
65 70 75 80	
ATG TTG GGT GGT TGT CCA AAA GAG CGT GCA GAG ATT TCA ATG CTT GAA	288
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu	

134

85								90				95				
GGA	GCG	GTT	TTG	GAT	ATT	AGA	TAC	GGT	GTT	TCG	AGA	ATT	GCA	TAT	AGT	336
Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser	
			100					105					110			
AAA	GAC	TTT	GAA	ACT	CTC	AAA	GTT	GAT	TTT	CTT	AGC	AAG	CTA	CCT	GAA	384
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu	
		115					120					125				
ATG	CTG	AAA	ATG	TTC	GAA	GAT	CGT	TTA	TGT	CAT	AAA	ACA	TAT	TTA	AAT	432
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn	
		130				135					140					
GGT	GAT	CAT	GTA	ACC	CAT	CCT	GAC	TTC	ATG	TTG	TAT	GAC	GCT	CTT	GAT	480
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp	
145					150					155				160		
GTT	GTT	TTA	TAC	ATG	GAC	CCA	ATG	TGC	CTG	GAT	GCG	TTC	CCA	AAA	TTA	528
Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu	
				165				170						175		
GTT	TGT	TTT	AAA	AAA	CGT	ATT	GAA	GCT	ATC	CCA	CAA	ATT	GAT	AAG	TAC	576
Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr	
			180				185						190			
TTG	AAA	TCC	AGC	AAG	TAT	ATA	GCA	TGG	CCT	TTG	CAG	GGC	TGG	CAA	GCC	624
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala	
		195					200					205				
ACG	TTT	GGT	GGT	GGC	GAC	CAT	CCT	CCA	AAA	TCG	GAT	CTG	ATC	GAA	GGT	672
Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Ile	Glu	Gly	
		210				215					220					
CGT	GGG	ATC	CCC	AAT	TCG	AGC	TCG	GTA	CCC	ATG	AGC	ACG	ATT	CCC	AAA	720
Arg	Gly	Ile	Pro	Asn	Ser	Ser	Ser	Val	Pro	Met	Ser	Thr	Ile	Pro	Lys	
225					230					235					240	
CCT	CAA	AGA	AAA	ACC	AAA	CGT	AAC	ACC	AAC	CGT	CGC	CCA	CAG	GAC	GTC	768
Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn	Thr	Asn	Arg	Arg	Pro	Gln	Asp	Val	
				245				250						255		
AAG	TTC	CCG	GGT	GGC	GGT	CAG	ATC	GTT	GGT	GGA	GTT	TAC	TTG	TTG	CCG	816
Lys	Phe	Pro	Gly	Gly	Gly	Gln	Ile	Val	Gly	Gly	Val	Tyr	Leu	Leu	Pro	
			260					265					270			
CGC	AGG	GGC	CCT	AGA	TTG	GGT	GTG	CGC	GCG	ACG	AGG	AAG	ACT	TCC	GAG	864
Arg	Arg	Gly	Pro	Arg	Leu	Gly	Val	Arg	Ala	Thr	Arg	Lys	Thr	Ser	Glu	
		275				280						285				
CGG	TCG	CAA	CCT	CGA	GGT	AGA	CGT	CAG	CCT	ATC	CCC	AAG	GCA	CGT	CGG	912
Arg	Ser	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	Ile	Pro	Lys	Ala	Arg	Arg	

135

290	295	300	948
CCC GAG GGC AGG ACG GGG ATC GGG AAT TCA TCG TGA			
Pro Glu Gly Arg Thr Gly Ile Gly Asn Ser Ser			
305	310	315	

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 759 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG TCC CCT ATA CTA GGT TAT TGG AAA ATT AAG GGC CTT GTG CAA CCC	48
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro	
1 5 10 15	
ACT CGA CTT CTT TTG GAA TAT CTT GAA GAA AAA TAT GAA GAG CAT TTG	96
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu	
20 25 30	
TAT GAG CGC GAT GAA GGT GAT AAA TGG CGA AAC AAA AAG TTT GAA TTG	144
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu	
35 40 45	
GGT TTG GAG TTT CCC AAT CTT CCT TAT TAT ATT GAT GGT GAT GTT AAA	192
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys	
50 55 60	
TTA ACA CAG TCT ATG GCC ATC ATA CGT TAT ATA GCT GAC AAG CAC AAC	240
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn	
65 70 75 80	
ATG TTG GGT GGT TGT CCA AAA GAG CGT GCA GAG ATT TCA ATG CTT GAA	288
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu	
85 90 95	

136

GGA GCG GTT TTG GAT ATT AGA TAC GGT GTT TCG AGA ATT GCA TAT AGT	336
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser	
100 105 110	
AAA GAC TTT GAA ACT CTC AAA GTT GAT TTT CTT AGC AAG CTA CCT GAA	384
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu	
115 120 125	
ATG CTG AAA ATG TTC GAA GAT CGT TTA TGT CAT AAA ACA TAT TTA AAT	432
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn	
130 135 140	
GGT GAT CAT GTA ACC CAT CCT GAC TTC ATG TTG TAT GAC GCT CTT GAT	480
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp	
145 150 155 160	
GTT GTT TTA TAC ATG GAC CCA ATG TGC CTG GAT GCG TTC CCA AAA TTA	528
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu	
165 170 175	
GTT TGT TTT AAA AAA CGT ATT GAA GCT ATC CCA CAA ATT GAT AAG TAC	576
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr	
180 185 190	
TTG AAA TCC AGC AAG TAT ATA GCA TGG CCT TTG CAG GGC TGG CAA GCC	624
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala	
195 200 205	
ACG TTT GGT GGT GGC GAC CAT CCT CCA AAA TCG GAT CTG GTT CCG CGT	672
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg	
210 215 220	
GGA TCC ATG AGC ACG ATT CCC AAA CCT CAA AGA AAA ACC AAA CGT AAC	720
Gly Ser Met Ser Thr Ile Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn	
225 230 235 240	
ACC AAC CGT CGC CCA CAG GAA TTC ATC GTG ACT GAC TGA	759
Thr Asn Arg Arg Pro Gln Glu Phe Ile Val Thr Asp	
245 250	

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 759 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATG	TCC	CCT	ATA	CTA	GGT	TAT	TGG	AAA	ATT	AAG	GGC	CTT	GTG	CAA	CCC	48
Met	Ser	Pro	Ile	Leu	Gly	Tyr	Trp	Lys	Ile	Lys	Gly	Leu	Val	Gln	Pro	
1				5				10						15		
ACT	CGA	CTT	CTT	TTG	GAA	TAT	CTT	GAA	GAA	AAA	TAT	GAA	GAG	CAT	TTG	96
Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	Glu	Glu	His	Leu	
			20					25					30			
TAT	GAG	CGC	GAT	GAA	GGT	GAT	AAA	TGG	CGA	AAC	AAA	AAG	TTT	GAA	TTG	144
Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu	
		35					40					45				
GGT	TTG	GAG	TTT	CCC	AAT	CTT	CCT	TAT	TAT	ATT	GAT	GGT	GAT	GTT	AAA	192
Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys	
	50					55					60					
TTA	ACA	CAG	TCT	ATG	GCC	ATC	ATA	CGT	TAT	ATA	GCT	GAC	AAG	CAC	AAC	240
Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn	
65					70				75						80	
ATG	TTG	GGT	GGT	TGT	CCA	AAA	GAG	CGT	GCA	GAG	ATT	TCA	ATG	CTT	GAA	288
Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu	
				85					90					95		
GGA	GCG	GTT	TTG	GAT	ATT	AGA	TAC	GGT	GTT	TCG	AGA	ATT	GCA	TAT	AGT	336
Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser	
			100					105					110			
AAA	GAC	TTT	GAA	ACT	CTC	AAA	GTT	GAT	TTT	CTT	AGC	AAG	CTA	CCT	GAA	384
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu	
		115					120					125				
ATG	CTG	AAA	ATG	TTC	GAA	GAT	CGT	TTA	TGT	CAT	AAA	ACA	TAT	TTA	AAT	432
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn	
	130					135					140					
GGT	GAT	CAT	GTA	ACC	CAT	CCT	GAC	TTC	ATG	TTG	TAT	GAC	GCT	CTT	GAT	480
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp	
145					150					155					160	

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GTT GTT TTA TAC ATG GAC CCA ATG TGC CTG GAT GCG TTC CCA AAA TTA	528
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu	
165 170 175	
GTT TGT TTT AAA AAA CGT ATT GAA GCT ATC CCA CAA ATT GAT AAG TAC	576
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr	
180 185 190	
TTG AAA TCC AGC AAG TAT ATA GCA TGG CCT TTG CAG GGC TGG CAA GCC	624
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala	
195 200 205	
ACG TTT GGT GGT GGC GAC CAT CCT CCA AAA TCG GAT CTG GTT CCG CGT	672
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg	
210 215 220	
GGA TCC GAC GTC AAG TTC CCG GGT GGC GGT CAG ATC GTT GGT GGA GTT	720
Gly Ser Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly Gly Val	
225 230 235 240	
TAC TTG TTG CCG CGC AGG GAA TTC ATC GTG ACT GAC TGA	759
Tyr Leu Leu Pro Arg Arg Glu Phe Ile Val Thr Asp	
245 250	

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 759 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG TCC CCT ATA CTA GGT TAT TGG AAA ATT AAG GGC CTT GTG CAA CCC	48
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro	
1 5 10 15	
ACT CGA CTT CTT TTG GAA TAT CTT GAA GAA AAA TAT GAA GAG CAT TTG	96

139

Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	Glu	Glu	His	Leu	
			20					25					30			
TAT	GAG	CGC	GAT	GAA	GGT	GAT	AAA	TGG	CGA	AAC	AAA	AAG	TTT	GAA	TTG	144
Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu	
		35					40					45				
GGT	TTG	GAG	TTT	CCC	AAT	CTT	CCT	TAT	TAT	ATT	GAT	GGT	GAT	GTT	AAA	192
Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys	
	50					55					60					
TTA	ACA	CAG	TCT	ATG	GCC	ATC	ATA	CGT	TAT	ATA	GCT	GAC	AAG	CAC	AAC	240
Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn	
	65				70					75					80	
ATG	TTG	GGT	GGT	TGT	CCA	AAA	GAG	CGT	GCA	GAG	ATT	TCA	ATG	CTT	GAA	288
Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu	
				85				90						95		
GGA	GCG	GTT	TTG	GAT	ATT	AGA	TAC	GGT	GTT	TCG	AGA	ATT	GCA	TAT	AGT	336
Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser	
			100					105					110			
AAA	GAC	TTT	GAA	ACT	CTC	AAA	GTT	GAT	TTT	CTT	AGC	AAG	CTA	CCT	GAA	384
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu	
		115					120					125				
ATG	CTG	AAA	ATG	TTC	GAA	GAT	CGT	TTA	TGT	CAT	AAA	ACA	TAT	TTA	AAT	432
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn	
	130					135					140					
GGT	GAT	CAT	GTA	ACC	CAT	CCT	GAC	TTC	ATG	TTG	TAT	GAC	GCT	CTT	GAT	480
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp	
	145				150					155					160	
GTT	GTT	TTA	TAC	ATG	GAC	CCA	ATG	TGC	CTG	GAT	GCG	TTC	CCA	AAA	TTA	528
Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu	
				165				170						175		
GTT	TGT	TTT	AAA	AAA	CGT	ATT	GAA	GCT	ATC	CCA	CAA	ATT	GAT	AAG	TAC	576
Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr	
			180					185					190			
TTG	AAA	TCC	AGC	AAG	TAT	ATA	GCA	TGG	CCT	TTG	CAG	GGC	TGG	CAA	GCC	624
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala	
		195					200					205				
ACG	TTT	GGT	GGT	GGC	GAC	CAT	CCT	CCA	AAA	TCG	GAT	CTG	GTT	CCG	CGT	672
Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg	
	210					215					220					
GGA	TCC	GGC	CCT	AGA	TTG	GGT	GTG	CGC	GCG	ACG	AGG	AAG	ACT	TCC	GAG	720

140

Gly Ser Gly Pro Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu
 225 230 235 240

CGG TCG CAA CCT CGA GGT GAA TTC ATC GTG ACT GAC TGA
 Arg Ser Gln Pro Arg Gly Glu Phe Ile Val Thr Asp
 245 250

759

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATG TCC CCT ATA CTA GGT TAT TGG AAA ATT AAG GGC CTT GTG CAA CCC	48
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro	
1 5 10 15	
ACT CGA CTT CTT TTG GAA TAT CTT GAA GAA AAA TAT GAA GAG CAT TTG	96
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu	
20 25 30	
TAT GAG CGC GAT GAA GGT GAT AAA TGG CGA AAC AAA AAG TTT GAA TTG	144
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu	
35 40 45	
GGT TTG GAG TTT CCC AAT CTT CCT TAT TAT ATT GAT GGT GAT GTT AAA	192
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys	
50 55 60	
TTA ACA CAG TCT ATG GCC ATC ATA CGT TAT ATA GCT GAC AAG CAC AAC	240
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn	
65 70 75 80	
ATG TTG GGT GGT TGT CCA AAA GAG CGT GCA GAG ATT TCA ATG CTT GAA	288
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu	

141																	
85								90				95					
GGA	GCG	GTT	TTG	GAT	ATT	AGA	TAC	GGT	GTT	TCG	AGA	ATT	GCA	TAT	AGT	336	
Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser		
			100				105			110							
AAA	GAC	TTT	GAA	ACT	CTC	AAA	GTT	GAT	TTT	CTT	AGC	AAG	CTA	CCT	GAA	384	
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu		
		115					120				125						
ATG	CTG	AAA	ATG	TTC	GAA	GAT	CGT	TTA	TGT	CAT	AAA	ACA	TAT	TTA	AAT	432	
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn		
		130					135				140						
GGT	GAT	CAT	GTA	ACC	CAT	CCT	GAC	TTC	ATG	TTG	TAT	GAC	GCT	CTT	GAT	480	
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp		
		145			150				155				160				
GTT	GTT	TTA	TAC	ATG	GAC	CCA	ATG	TGC	CTG	GAT	GCG	TTC	CCA	AAA	TTA	528	
Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu		
				165					170				175				
GTT	TGT	TTT	AAA	AAA	CGT	ATT	GAA	GCT	ATC	CCA	CAA	ATT	GAT	AAG	TAC	576	
Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr		
		180						185				190					
TTG	AAA	TCC	AGC	AAG	TAT	ATA	GCA	TGG	CCT	TTG	CAG	GGC	TGG	CAA	GCC	624	
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala		
		195				200						205					
ACG	TTT	GGT	GGT	GGC	GAC	CAT	CCT	CCA	AAA	TCG	GAT	CTG	GTT	CCG	CGT	672	
Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg		
		210				215				220							
GGA	TCC	AGC	ACG	ATT	CCC	AAA	CCT	CAA	AGA	AAA	ACC	AAA	CGT	AAC	ACC	720	
Gly	Ser	Ser	Thr	Ile	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn	Thr		
		225		230				235				240					
AAC	CGT	CGC	CCA	CAG	GAC	GTC	AAG	TTC	CCG	GGT	GGC	GGT	CAG	ATC	GTT	768	
Asn	Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly	Gln	Ile	Val		
				245				250						255			
GGT	GGA	GTT	TAC	TTG	TTG	CCG	CGC	AGG	GAA	TTC	ATC	GTG	ACT	GAC		813	
Gly	Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Glu	Phe	Ile	Val	Thr	Asp			
		260						265				270					
TGA																	816

(2) INFORMATION FOR SEQ ID NO:7:

(1) SEQUENCE CHARACTERISTICS:

142

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GATCCATGAG CACGATTCCC AAACCTCAAA GAAAACCAA ACGTAACACC AACCGTCGCC 60

CACAGG 66

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AATTCCTGTG GGCGACGGTT GGTGTTACGT TTGGTTTTTC TTTGAGGTTT GGGAATCGTG 60

CTCATG 66

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

143

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GATCCGACGT CAAGTTCCCG GGTGGCGGTC AGATCGTTGG TGGAGTTTAC TTGTTGCCGC 60
GCAGGG 66

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AATTCCTGC GCGGCAACAA GTAACTCCA CCAACGATCT GACCGCCACC CGGGAAGTTG 60
ACGTCG 66

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GATCCGGCCC TAGATTGGGT GTGCGCGCGA CGAGGAAGAC TTCCGAGCGG TCGCAACCTC 60

144

GAGGTG

66

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AATTCACCTC GAGGTTGCGA CCGCTCGGAA GTCTTCCTCG TCGCGCGCAC ACCCAATCTA

60

GGGCCG

66

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAATTCTTAC CTGCGCGGCA ACAAGTAAAC TC

32

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

145

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCTGGATCCA GCACGATTCC CAAACCTCAA AG

32

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ATGAGCACGA TTCCCAAACC T

21

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAGGAAGACT TCCGAGC

17

146

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTCCTGCCCT CGGGCCG

17

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ACCCAAATTG CGCGACCTAC G

21

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

147

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TGGGTAAGGT CATCGATAC

19

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

AAGGTCATCG ATACCCT

17

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AGATAGAGAA AGAGCAAC

18

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

148

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GGACCAGTTC ATCATCATAT AT

22

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CAGTTCATCA TCATATCCCA

20

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

149

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..15
- (D) OTHER INFORMATION: /product= "Linker Protein in GST-NANBV 693-691"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GGG ATC CCC AAT TCA
Gly Ile Pro Asn Ser
1 5

15

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Gly Ile Pro Asn Ser
1 5

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..9
- (D) OTHER INFORMATION: /product= "Carboxy-terminal Linker Protein in GST-NANBV 693-691"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

150

AAT TCA TCG TGA
Asn Ser Ser
1

12

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Asn Ser Ser
1

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..27
- (D) OTHER INFORMATION: /product= "Linker Protein in
GST-NANBV 15-18"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GGG ATC CCC ATC GAA TTC CTG CAG CCC
Gly Ile Pro Ile Glu Phe Leu Gln Pro
1 5

27

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids

151

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Gly Ile Pro Ile Glu Phe Leu Gln Pro
1 5

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..21
(D) OTHER INFORMATION: /product= "Carboxy-terminal Linker
Protein in GST-NANBV 15-18"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TGG GGG ATC GGG AAT TCA TCG TGA
Trp Gly Ile Gly Asn Ser Ser
1 5

24

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Trp Gly Ile Gly Asn Ser Ser
1 5

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..24
- (D) OTHER INFORMATION: /product= "Linker Protein in GST-NANBV 15-17"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GGG ATC CCC AAT TCC TGC AGC CCT
Gly Ile Pro Asn Ser Cys Ser Pro
1 5

24

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Gly Ile Pro Asn Ser Cys Ser Pro
1 5

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

153

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..18

(D) OTHER INFORMATION: /product= "Carboxy-terminal Linker
Protein in GST-NANBV 15-17"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GGG ATC GGG AAT TCA TCG TGA
Gly Ile Gly Asn Ser Ser
1 5

21

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Gly Ile Gly Asn Ser Ser
1 5

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

154

- (B) LOCATION: 1..15
- (D) OTHER INFORMATION: /product= "Thrombin Cleavage Site
in GST-NANBV 15-17"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GTT CCG CGT GGA TCC
Val Pro Arg Gly Ser
1 5

15

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Val Pro Arg Gly Ser
1 5

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /product= "Linker Protein in
GST-NANBV 15-17"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CCA TCG AAT TCC TGC AGC CCT
Pro Ser Asn Ser Cys Ser Pro

21

155

1

5

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Pro Ser Asn Ser Cys Ser Pro
1 5

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..15
- (D) OTHER INFORMATION: /product= "Carboxy-terminal Linker Protein in GST-NANBV 15-17"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GGA ATT CAT CGT GAC TGA
Gly Ile His Arg Asp
1 5

18

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

156

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Gly Ile His Arg Asp
1 5

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..27
- (D) OTHER INFORMATION: /product= "Linker Protein in GST-NANBV 690-691"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GGG ATC CCC AAT TCG AGC TCG GTA CCC
Gly Ile Pro Asn Ser Ser Ser Val Pro
1 5

27

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Gly Ile Pro Asn Ser Ser Ser Val Pro
1 5

(2) INFORMATION FOR SEQ ID NO:44:

157

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /product= "Carboxy-terminal Linker Protein in GST-NANBV 690-691"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ACG GGG ATC GGG AAT TCA TCG TGA
Thr Gly Ile Gly Asn Ser Ser
1 5

24

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Thr Gly Ile Gly Asn Ser Ser
1 5

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9416 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 342..9374

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..12
- (D) OTHER INFORMATION: /note= "Not confirmed as HCV-Hc59 Sequence"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 9397..9416
- (D) OTHER INFORMATION: /note= "Not confirmed as HCV-Hc59 Sequence"

(ix) FEATURE:

- (A) NAME/KEY: repeat_unit
- (B) LOCATION: group(7..12, 42..47)
- (D) OTHER INFORMATION: /rpt_type= "other"
/rpt_family= "1"

(ix) FEATURE:

- (A) NAME/KEY: repeat_unit
- (B) LOCATION: group(23..28, 38..43, 9209..9214, 9391..9396)
- (D) OTHER INFORMATION: /rpt_type= "other"
/rpt_family= "2"

(ix) FEATURE:

- (A) NAME/KEY: repeat_unit
- (B) LOCATION: group(128..135, 315..322)
- (D) OTHER INFORMATION: /rpt_type= "other"
/rpt_family= "3"

(ix) FEATURE:

- (A) NAME/KEY: repeat_unit
- (B) LOCATION: group(9231..9237, 9245..9251, 9256..9262)
- (D) OTHER INFORMATION: /rpt_type= "other"
/rpt_family= "4"

(ix) FEATURE:

- (A) NAME/KEY: repeat_unit
- (B) LOCATION: group(9248..9253, 9221..9226, 9227..9232)
- (D) OTHER INFORMATION: /rpt_type= "other"
/rpt_family= "5"

159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GCCAGCCCCC	TGATGGGGGC	GACACTCCAC	CATGAATCAC	TCCCCTGTGA	GGAACACTG	60
TCTTCACGCA	GAAAGCGTCT	AGCCATGGCG	TTAGTATGAG	TGTCGTGCAG	CCTCCAGGAC	120
CCCCCCTCCC	GGGAGAGCCA	TAGTGGTCTG	CGGAACCGGT	GAGTACACCG	GAATTGCCAG	180
GACGACCGGG	TCCTTTCTTG	GATAAACCCG	CTCAATGCCT	GGAGATTGG	GCGTGCCCCC	240
GCAAGACTGC	TAGCCGAGTA	GTGTTGGGTC	GCGAAAGGCC	TTGTGGTACT	GCCTGATAGG	300
GTGCTTGCGA	GTGCCCCGGG	AGGTCTCGTA	GACCGTGCAC	C ATG AGC ACG AAT		353
				Met Ser Thr Asn		
				1		
CCT AAA CCT CAA AGA AAA ACC AAA CGT AAC ACC AAC CGT CGC CCA CAG	401					
Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn Arg Arg Pro Gln						
5 10 15 20						
GAC GTC AAG TTC CCG GGT GGC GGT CAG ATC GTT GGT GGA GTT TAC TTG	449					
Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly Gly Val Tyr Leu						
25 30 35						
TTG CCG CGC AGG GGC CCT AGA TTG GGT GTG CGC GCG ACG AGG AAG ACT	497					
Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala Thr Arg Lys Thr						
40 45 50						
TCC GAG CGG TCG CAA CCT CGA GGT AGA CGT CAG CCT ATC CCC AAG GCA	545					
Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala						
55 60 65						
CGT CGG CCC GAG GGC AGG ACC TGG GCT CAG CCC GGG TAC CCT TGG CCC	593					
Arg Arg Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly Tyr Pro Trp Pro						
70 75 80						
CTC TAT GGC AAT GAG GGT TGC GGG TGG GCG GGA TGG CTC CTG TCT CCC	641					
Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu Ser Pro						
85 90 95 100						
CGT GGC TCT CGG CCT AGC TGG GGC CCC ACA GAC CCC CGG CGT AGG TCG	689					
Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro Arg Arg Arg Ser						
105 110 115						
CGC AAT TTG GGT AAG GTC ATC GAT ACC CTT ACG TGC GGC TTC GCC GAC	737					
Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Ala Asp						
120 125 130						
CTC ATG GGG TAC ATA CCG CTC GTC GGC GCC CCT CTT GGA GGC GCT GCC	785					
Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Gly Gly Ala Ala						
135 140 145						

160

AGG	GCC	CTG	GCG	CAT	GGC	GTC	CGG	GTT	CTG	GAA	GAC	GGC	GTG	AAC	TAT	833
Arg	Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	
	150					155					160					
GCA	ACA	GGG	AAC	CTT	CCT	GGT	TGC	TCT	TTC	TCT	ATC	TTC	CTT	CTG	GCC	881
Ala	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	
	165				170					175					180	
CTG	CTC	TCT	TGC	CTG	ACT	GTG	CCC	GCT	TCA	GCC	TAC	CAA	GTG	CGC	AAT	929
Leu	Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala	Tyr	Gln	Val	Arg	Asn	
				185					190					195		
TCC	TCG	GGG	CTT	TAC	CAT	GTC	ACC	AAT	GAT	TGC	CCT	AAC	TCG	AGT	GTT	977
Ser	Ser	Gly	Leu	Tyr	His	Val	Thr	Asn	Asp	Cys	Pro	Asn	Ser	Ser	Val	
			200					205					210			
GTG	TAC	GAG	GCG	GCC	GAT	GCC	ATC	CTG	CAC	ACT	CCG	GGG	TGT	GTC	CCT	1025
Val	Tyr	Glu	Ala	Ala	Asp	Ala	Ile	Leu	His	Thr	Pro	Gly	Cys	Val	Pro	
		215					220					225				
TGC	GTT	CGC	GAG	GGT	AAC	GCC	TCG	AGG	TGT	TGG	GTG	GCG	GTG	ACC	CCC	1073
Cys	Val	Arg	Glu	Gly	Asn	Ala	Ser	Arg	Cys	Trp	Val	Ala	Val	Thr	Pro	
	230					235					240					
ACG	GTG	GCC	ACC	AGG	GAC	GGC	AAA	CTC	CCC	ACA	ACG	CAG	CTT	CGA	CGT	1121
Thr	Val	Ala	Thr	Arg	Asp	Gly	Lys	Leu	Pro	Thr	Thr	Gln	Leu	Arg	Arg	
	245				250					255					260	
CAT	ATC	GAT	CTG	CTT	GTC	GGG	AGC	GCC	ACC	CTC	TGC	TCG	GCC	CTC	TAC	1169
His	Ile	Asp	Leu	Leu	Val	Gly	Ser	Ala	Thr	Leu	Cys	Ser	Ala	Leu	Tyr	
				265					270					275		
GTG	GGG	GAC	CTG	TGC	GGG	TCT	GTC	TTT	CTT	GTT	GGT	CAA	CTG	TTT	ACC	1217
Val	Gly	Asp	Leu	Cys	Gly	Ser	Val	Phe	Leu	Val	Gly	Gln	Leu	Phe	Thr	
			280					285					290			
TTC	TCT	CCC	AGG	CAC	CAC	TGG	ACG	ACG	CAA	GAC	TGC	AAT	TGT	TCT	ATC	1265
Phe	Ser	Pro	Arg	His	His	Trp	Thr	Thr	Gln	Asp	Cys	Asn	Cys	Ser	Ile	
		295				300						305				
TAT	CCC	GGC	CAT	ATA	ACG	GGT	CAT	CGC	ATG	GCA	TGG	AAT	ATG	ATG	ATG	1313
Tyr	Pro	Gly	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asn	Met	Met	Met	
	310					315					320					
AAC	TGG	TCC	CCT	ACG	GCA	GCG	TTG	GTG	GTA	GCT	CAG	CTG	CTC	CGA	ATC	1361
Asn	Trp	Ser	Pro	Thr	Ala	Ala	Leu	Val	Val	Ala	Gln	Leu	Leu	Arg	Ile	
	325				330					335					340	
CCA	CAA	GCC	ATC	ATG	GAC	ATG	ATC	GCT	GGC	GCC	CAC	TGG	GGA	GTC	CTG	1409
Pro	Gln	Ala	Ile	Met	Asp	Met	Ile	Ala	Gly	Ala	His	Trp	Gly	Val	Leu	
				345					350					355		

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GCG	GGC	ATA	AAG	TAT	TTC	TCC	ATG	GTG	GGG	AAC	TGG	GCG	AAG	GTC	CTG	1457
Ala	Gly	Ile	Lys	Tyr	Phe	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val	Leu	
			360					365					370			
GTA	GTG	CTG	CTG	CTA	TTT	GCC	GGC	GTC	GAC	GCG	GAA	ACC	CAC	GTC	ACC	1505
Val	Val	Leu	Leu	Leu	Phe	Ala	Gly	Val	Asp	Ala	Glu	Thr	His	Val	Thr	
		375					380					385				
GGG	GGA	AAT	GCC	GGC	CGC	ACC	ACG	GCT	GGG	CTT	GTT	GGT	CTC	CTT	ACA	1553
Gly	Gly	Asn	Ala	Gly	Arg	Thr	Thr	Ala	Gly	Leu	Val	Gly	Leu	Leu	Thr	
	390					395					400					
CCA	GGC	GCC	AAG	CAG	AAC	ATC	CAA	CTG	ATC	AAC	ACC	AAC	GGC	AGT	TGG	1601
Pro	Gly	Ala	Lys	Gln	Asn	Ile	Gln	Leu	Ile	Asn	Thr	Asn	Gly	Ser	Trp	
405					410					415					420	
CAC	ATC	AAT	AGC	ACG	GCC	TTG	AAC	TGC	AAT	GAA	AGC	CTT	AAC	ACC	GGC	1649
His	Ile	Asn	Ser	Thr	Ala	Leu	Asn	Cys	Asn	Glu	Ser	Leu	Asn	Thr	Gly	
				425					430					435		
TGG	TTA	GCA	GGG	CTC	TTC	TAT	CAG	CAC	AAA	TTC	AAC	TCT	TCA	GGC	TGT	1697
Trp	Leu	Ala	Gly	Leu	Phe	Tyr	Gln	His	Lys	Phe	Asn	Ser	Ser	Gly	Cys	
			440					445					450			
CCT	GAG	AGG	TTG	GCC	AGC	TGC	CGA	CGC	CTT	ACC	GAT	TTT	GCC	CAG	GGC	1745
Pro	Glu	Arg	Leu	Ala	Ser	Cys	Arg	Arg	Leu	Thr	Asp	Phe	Ala	Gln	Gly	
		455					460					465				
TGG	GGT	CCT	ATC	AGT	TAT	GCC	AAC	GGA	AGC	GGC	CTC	GAC	GAA	CGC	CCC	1793
Trp	Gly	Pro	Ile	Ser	Tyr	Ala	Asn	Gly	Ser	Gly	Leu	Asp	Glu	Arg	Pro	
	470					475					480					
TAC	TGC	TGG	CAC	TAC	CCT	CCA	AGA	CCT	TGT	GGC	ATT	GTG	CCC	GCA	AAG	1841
Tyr	Cys	Trp	His	Tyr	Pro	Pro	Arg	Pro	Cys	Gly	Ile	Val	Pro	Ala	Lys	
485					490					495					500	
AGC	GTG	TGT	GGC	CCG	GTA	TAT	TGC	TTC	ACT	CCC	AGC	CCC	GTG	GTG	GTG	1889
Ser	Val	Cys	Gly	Pro	Val	Tyr	Cys	Phe	Thr	Pro	Ser	Pro	Val	Val	Val	
				505					510					515		
GGA	ACG	ACC	GAC	AGG	TCG	GGC	GCG	CCT	ACC	TAC	AGC	TGG	GGT	GCA	AAT	1937
Gly	Thr	Thr	Asp	Arg	Ser	Gly	Ala	Pro	Thr	Tyr	Ser	Trp	Gly	Ala	Asn	
			520				525						530			
GAT	ACG	GAT	GTC	TTC	GTC	CTT	AAC	AAC	ACC	AGG	CCA	CCG	CTG	GGC	AAT	1985
Asp	Thr	Asp	Val	Phe	Val	Leu	Asn	Asn	Thr	Arg	Pro	Pro	Leu	Gly	Asn	
		535					540					545				
TGG	TTC	GGT	TGT	ACC	TGG	ATG	AAC	TCA	ACT	GGA	TTC	ACC	AAA	GTG	TGC	2033
Trp	Phe	Gly	Cys	Thr	Trp	Met	Asn	Ser	Thr	Gly	Phe	Thr	Lys	Val	Cys	
	550					555					560					

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GGA GCG CCC CCT TGT GTC ATC GGA GGG GTG GGC AAC AAC ACC TTG CTC Gly Ala Pro Pro Cys Val Ile Gly Gly Val Gly Asn Asn Thr Leu Leu 565 570 575 580	2081
TGC CCC ACT GAT TGC TTC CGC AAA TAT CCG GAA GCC ACA TAC TCT CGG Cys Pro Thr Asp Cys Phe Arg Lys Tyr Pro Glu Ala Thr Tyr Ser Arg 585 590 595	2129
TGC GGC TCC GGT CCC AGG ATT ACA CCC AGG TGC ATG GTC GAC TAC CCG Cys Gly Ser Gly Pro Arg Ile Thr Pro Arg Cys Met Val Asp Tyr Pro 600 605 610	2177
TAT AGG CTT TGG CAC TAT CCT TGT ACC ATC AAT TAC ACC ATA TTC AAA Tyr Arg Leu Trp His Tyr Pro Cys Thr Ile Asn Tyr Thr Ile Phe Lys 615 620 625	2225
GTC AGG ATG TAC GTG GGA GGG GTC GAG CAC AGG CTG GAA GCG GCC TGC Val Arg Met Tyr Val Gly Gly Val Glu His Arg Leu Glu Ala Ala Cys 630 635 640	2273
AAC TGG ACG CGG GGC GAA CGC TGT GAT CTG GAA GAC AGG GAC AGG TCC Asn Trp Thr Arg Gly Glu Arg Cys Asp Leu Glu Asp Arg Asp Arg Ser 645 650 655 660	2321
GAG CTC AGC CCG TTG CTG CTG TCC ACC ACA CAG TGG CAG GTC CTT CCG Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Gln Trp Gln Val Leu Pro 665 670 675	2369
TGT TCT TTC ACG ACC CTG CCA GCC TTG TCC ACC GGC CTC ATC CAC CTC Cys Ser Phe Thr Thr Leu Pro Ala Leu Ser Thr Gly Leu Ile His Leu 680 685 690	2417
CAC CAG AAC ATT GTG GAC GTG CAG TAC TTG TAC GGG GTA GGG TCA AGC His Gln Asn Ile Val Asp Val Gln Tyr Leu Tyr Gly Val Gly Ser Ser 695 700 705	2465
ATC GCG TCT TGG GCC ATT AAG TGG GAG TAC GTC GTT CTC CTG TTC CTT Ile Ala Ser Trp Ala Ile Lys Trp Glu Tyr Val Val Leu Leu Phe Leu 710 715 720	2513
CTG CTT GCA GAC GCG CGC GTC TGT TCC TGC TTG TGG ATG ATG TTA CTC Leu Leu Ala Asp Ala Arg Val Cys Ser Cys Leu Trp Met Met Leu Leu 725 730 735 740	2561
ATA TCC CAA GCG GAG GCG GCT TTG GAG AAC CTC GTA ATA CTC AAT GCA Ile Ser Gln Ala Glu Ala Ala Leu Glu Asn Leu Val Ile Leu Asn Ala 745 750 755	2609
GCA TCC CTG GCC GGG ACG CAT GGT CTT GTG TCC TTC CTC GTG TTC TTC Ala Ser Leu Ala Gly Thr His Gly Leu Val Ser Phe Leu Val Phe Phe 760 765 770	2657

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TGC	TTT	GCG	TGG	TAT	CTG	AAG	GGT	AGG	TGG	GTG	CCC	GGA	GCG	GTC	TAC	2705
Cys	Phe	Ala	Trp	Tyr	Leu	Lys	Gly	Arg	Trp	Val	Pro	Gly	Ala	Val	Tyr	
		775					780					785				
GCC	CTC	TAC	GGG	ATG	TGG	CCT	CTC	CTC	CTG	CTC	CTG	CTG	GCG	TTG	CCT	2753
Ala	Leu	Tyr	Gly	Met	Trp	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Ala	Leu	Pro	
	790					795					800					
CAG	CGG	GCA	TAC	GCA	CTG	GAC	ACG	GAG	GTG	GCC	GCG	TCG	TGT	GGC	GGC	2801
Gln	Arg	Ala	Tyr	Ala	Leu	Asp	Thr	Glu	Val	Ala	Ala	Ser	Cys	Gly	Gly	
805					810					815					820	
GTT	GTT	CTT	GTC	GGG	TTA	ATG	GCG	CTG	ACT	CTG	TCG	CCA	TAT	TAC	AAG	2849
Val	Val	Leu	Val	Gly	Leu	Met	Ala	Leu	Thr	Leu	Ser	Pro	Tyr	Tyr	Lys	
				825					830					835		
CGC	TAT	ATC	AGC	TGG	TGC	ATG	TGG	TGG	CTT	CAG	TAT	TTT	CTG	ACC	AGA	2897
Arg	Tyr	Ile	Ser	Trp	Cys	Met	Trp	Trp	Leu	Gln	Tyr	Phe	Leu	Thr	Arg	
			840					845					850			
GTA	GAA	GCG	CAA	CTG	CAC	GTG	TGG	GTT	CCC	CCC	CTC	AAC	GTC	CGG	GGG	2945
Val	Glu	Ala	Gln	Leu	His	Val	Trp	Val	Pro	Pro	Leu	Asn	Val	Arg	Gly	
		855					860					865				
GGG	CGC	GAT	GCC	GTC	ATC	TTA	CTC	ACG	TGT	GTA	GTA	CAC	CCG	GCC	CTG	2993
Gly	Arg	Asp	Ala	Val	Ile	Leu	Leu	Thr	Cys	Val	Val	His	Pro	Ala	Leu	
	870					875					880					
GTA	TTT	GAC	ATC	ACC	AAA	CTA	CTC	CTG	GCC	ATC	TTC	GGA	CCC	CTT	TGG	3041
Val	Phe	Asp	Ile	Thr	Lys	Leu	Leu	Leu	Ala	Ile	Phe	Gly	Pro	Leu	Trp	
885					890					895					900	
ATT	CTT	CAA	GCC	AGT	TTG	CTT	AAA	GTC	CCC	TAC	TTC	GTG	CGC	GTT	CAA	3089
Ile	Leu	Gln	Ala	Ser	Leu	Leu	Lys	Val	Pro	Tyr	Phe	Val	Arg	Val	Gln	
				905					910					915		
GGC	CTT	CTC	CGG	ATC	TGC	GCG	CTA	GCG	CGG	AAG	ATA	GCC	GGA	GGT	CAT	3137
Gly	Leu	Leu	Arg	Ile	Cys	Ala	Leu	Ala	Arg	Lys	Ile	Ala	Gly	Gly	His	
			920					925					930			
TAC	GTG	CAA	ATG	GCC	ATC	ATC	AAG	TTA	GGG	GCG	CTT	ACT	GGC	ACC	TGT	3185
Tyr	Val	Gln	Met	Ala	Ile	Ile	Lys	Leu	Gly	Ala	Leu	Thr	Gly	Thr	Cys	
		935					940					945				
GTG	TAT	AAC	CAT	CTC	GCT	CCT	CTT	CGA	GAC	TGG	GCG	CAC	AAC	GGC	CTG	3233
Val	Tyr	Asn	His	Leu	Ala	Pro	Leu	Arg	Asp	Trp	Ala	His	Asn	Gly	Leu	
	950					955					960					
CGA	GAT	CTG	GCC	GTG	GCT	GTG	GAA	CCA	GTC	GTC	TTC	TCC	CGA	ATG	GAG	3281
Arg	Asp	Leu	Ala	Val	Ala	Val	Glu	Pro	Val	Val	Phe	Ser	Arg	Met	Glu	
965					970					975					980	

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ACC AAG CTC ATC ACG TGG GGG GCA GAT ACC GCC GCG TGC GGT GAC ATC Thr Lys Leu Ile Thr Trp Gly Ala Asp Thr Ala Ala Cys Gly Asp Ile 985 990 995	3329
ATC AAC GGC TTG CCC GTC TCT GCC CGT AGG GGC CAG GAG ATA CTG CTT Ile Asn Gly Leu Pro Val Ser Ala Arg Arg Gly Gln Glu Ile Leu Leu 1000 1005 1010	3377
GGG CCA GCC GAC GGA ATG GTC TCC AAG GGG TGG AGG TTG CTG GCG CCC Gly Pro Ala Asp Gly Met Val Ser Lys Gly Trp Arg Leu Leu Ala Pro 1015 1020 1025	3425
ATC ACG GCG TAC GCC CAG CAG ACG AGA GGC CTC CTA GGG TGT ATA ATC Ile Thr Ala Tyr Ala Gln Gln Thr Arg Gly Leu Leu Gly Cys Ile Ile 1030 1035 1040	3473
ACC AGC CTG ACT GGC CGG GAC AAA AAC CAA GTG GAG GGT GAG GTC CAG Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu Gly Glu Val Gln 1045 1050 1055 1060	3521
ATC GTG TCA ACT GCT ACC CAG ACC TTC CTG GCA ACG TGC ATC AAT GGG Ile Val Ser Thr Ala Thr Gln Thr Phe Leu Ala Thr Cys Ile Asn Gly 1065 1070 1075	3569
GTA TGC TGG ACT GTC TAC CAC GGG GCC GGA ACG AGG ACC ATC GCA TCA Val Cys Trp Thr Val Tyr His Gly Ala Gly Thr Arg Thr Ile Ala Ser 1080 1085 1090	3617
CCC AAG GGT CCT GTC ATC CAG ACG TAT ACC AAT GTG GAT CAA GAC CTC Pro Lys Gly Pro Val Ile Gln Thr Tyr Thr Asn Val Asp Gln Asp Leu 1095 1100 1105	3665
GTG GGC TGG CCC GCT CCT CAA GGT TCC CGC TCA TTG ACA CCC TGC ACC Val Gly Trp Pro Ala Pro Gln Gly Ser Arg Ser Leu Thr Pro Cys Thr 1110 1115 1120	3713
TGC GGC TCC TCG GAC CTT TAC CTG GTC ACG AGG CAC GCC GAT GTC ATT Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala Asp Val Ile 1125 1130 1135 1140	3761
CCC GTG CGC CGG CGA GGT GAT AGC AGG GGT AGC CTG CTT TCG CCC CGG Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu Ser Pro Arg 1145 1150 1155	3809
CCC ATT TCC TAC TTG AAA GGC TCC TCG GGG GGT CCG CTG TTG TGC CCC Pro Ile Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu Leu Cys Pro 1160 1165 1170	3857
ACG GGA CAC GCC GTG GGC CTA TTC AGG GCC GCG GTG TGC ACC CGT GGA Thr Gly His Ala Val Gly Leu Phe Arg Ala Ala Val Cys Thr Arg Gly 1175 1180 1185	3905

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GTG	GCT	AAG	GCG	GTG	GAC	TTT	ATC	CCT	GTG	GAG	AAC	CTA	GAG	ACA	ACC	3953
Val	Ala	Lys	Ala	Val	Asp	Phe	Ile	Pro	Val	Glu	Asn	Leu	Glu	Thr	Thr	
1190						1195					1200					
ATG	AGA	TCC	CCG	GTG	TTC	ACG	GAC	AAC	TCC	TCT	CCA	CCA	GCA	GTG	CCC	4001
Met	Arg	Ser	Pro	Val	Phe	Thr	Asp	Asn	Ser	Ser	Pro	Pro	Ala	Val	Pro	
1205					1210					1215					1220	
CAG	AGC	TTC	CAG	GTG	GCC	CAC	CTG	CAT	GCT	CCC	ACC	GGC	AGC	GGT	AAG	4049
Gln	Ser	Phe	Gln	Val	Ala	His	Leu	His	Ala	Pro	Thr	Gly	Ser	Gly	Lys	
				1225					1230					1235		
AGC	ACC	AAG	GTC	CCG	GCT	GCG	TAC	GCA	GCC	AAG	GGC	TAC	AAG	GTG	TTG	4097
Ser	Thr	Lys	Val	Pro	Ala	Ala	Tyr	Ala	Ala	Lys	Gly	Tyr	Lys	Val	Leu	
			1240					1245					1250			
GTG	CTC	AAC	CCC	TCT	GTT	GCT	GCA	ACA	CTG	GGC	TTT	GGT	GCT	TAC	ATG	4145
Val	Leu	Asn	Pro	Ser	Val	Ala	Ala	Thr	Leu	Gly	Phe	Gly	Ala	Tyr	Met	
		1255					1260					1265				
TCC	AAG	GCC	CAT	GGG	GTT	GAT	CCT	AAT	ATC	AGG	ACC	GGG	GTG	AGA	ACA	4193
Ser	Lys	Ala	His	Gly	Val	Asp	Pro	Asn	Ile	Arg	Thr	Gly	Val	Arg	Thr	
		1270				1275					1280					
ATT	ACC	ACT	GGC	AGC	CCC	ATC	ACG	TAC	TCC	ACC	TAC	GGC	AAG	TTC	CTT	4241
Ile	Thr	Thr	Gly	Ser	Pro	Ile	Thr	Tyr	Ser	Thr	Tyr	Gly	Lys	Phe	Leu	
1285					1290					1295					1300	
GCC	GAC	GCC	GGG	TGC	TCA	GGA	GGT	GCT	TAT	GAC	ATA	ATA	ATT	TGT	GAC	4289
Ala	Asp	Ala	Gly	Cys	Ser	Gly	Gly	Ala	Tyr	Asp	Ile	Ile	Ile	Cys	Asp	
				1305					1310					1315		
GAG	TGC	CAC	TCC	ACG	GAT	GCC	ACA	TCC	ATC	TCG	GGC	ATC	GGC	ACT	GTC	4337
Glu	Cys	His	Ser	Thr	Asp	Ala	Thr	Ser	Ile	Ser	Gly	Ile	Gly	Thr	Val	
			1320					1325					1330			
CTT	GAC	CAA	GCA	GAG	ACT	GCG	GGG	GCG	AGA	CTG	GTT	GTG	CTC	GCC	ACT	4385
Leu	Asp	Gln	Ala	Glu	Thr	Ala	Gly	Ala	Arg	Leu	Val	Val	Leu	Ala	Thr	
			1335				1340					1345				
GCT	ACC	CCT	CCG	GGC	TCC	GTC	ACT	GTG	TCC	CAT	CCT	AAC	ATC	GAG	GAG	4433
Ala	Thr	Pro	Pro	Gly	Ser	Val	Thr	Val	Ser	His	Pro	Asn	Ile	Glu	Glu	
			1350			1355					1360					
GTT	GCT	CTG	TCC	ACC	ACC	GGA	GAG	ATC	CCC	TTT	TAC	GGC	AAG	GCT	ATC	4481
Val	Ala	Leu	Ser	Thr	Thr	Gly	Glu	Ile	Pro	Phe	Tyr	Gly	Lys	Ala	Ile	
1365					1370					1375					1380	
CCC	CTC	GAG	GTG	ATC	AAG	GGG	GGA	AGA	CAT	CTC	ATC	TTC	TGC	CAC	TCA	4529
Pro	Leu	Glu	Val	Ile	Lys	Gly	Gly	Arg	His	Leu	Ile	Phe	Cys	His	Ser	
				1385					1390					1395		

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AAG AAG AAG TGC GAC GAG CTC GCC GCG AAG CTG GTC GCA TTG GGC ATC Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu Val Ala Leu Gly Ile 1400 1405 1410	4577
AAT GCC GTG GCC TAC TAC CGC GGT CTT GAC GTG TCT GTC ATC CCG ACC Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val Ile Pro Thr 1415 1420 1425	4625
AGC GGC GAT GTT GTC GTC GTG TCG ACC GAT GCT CTC ATG ACT GGC TTT Ser Gly Asp Val Val Val Val Ser Thr Asp Ala Leu Met Thr Gly Phe 1430 1435 1440	4673
ACC GGC GAC TTC GAC TCT GTG ATA GAC TGC AAC ACG TGT GTC ACT CAG Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Thr Cys Val Thr Gln 1445 1450 1455 1460	4721
ACA GTC GAT TTT AGC CTT GAC CCT ACC TTT ACC ATT GAG ACA ACC ACG Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr Thr 1465 1470 1475	4769
CTC CCC CAG GAT GCT GTC TCC AGG ACT CAA CGC CGG GGC AGG ACT GGC Leu Pro Gln Asp Ala Val Ser Arg Thr Gln Arg Arg Gly Arg Thr Gly 1480 1485 1490	4817
AGG GGG AAG CCA GGC ATC TAT AGA TTT GTG GCA CCG GGG GAG CGC CCC Arg Gly Lys Pro Gly Ile Tyr Arg Phe Val Ala Pro Gly Glu Arg Pro 1495 1500 1505	4865
TCC GGC ATG TTC GAC TCG TCC GTC CTC TGT GAG TGC TAT GAC GCG GGC Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu Cys Tyr Asp Ala Gly 1510 1515 1520	4913
TGT GCT TGG TAT GAG CTC ACG CCC GCC GAG ACT ACA GTT AGG CTA CGA Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr Thr Val Arg Leu Arg 1525 1530 1535 1540	4961
GCG TAC ATG AAC ACC CCG GGG CTT CCC GTG TGC CAG GAC CAT CTT GGA Ala Tyr Met Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu Gly 1545 1550 1555	5009
TTT TGG GAG GGC GTC TTT ACG GGC CTC ACT CAT ATA GAT GCC CAC TTT Phe Trp Glu Gly Val Phe Thr Gly Leu Thr His Ile Asp Ala His Phe 1560 1565 1570	5057
CTA TCC CAG ACA AAG CAG AGT GGG GAG AAC TTT CCT TAC CTG GTA GCG Leu Ser Gln Thr Lys Gln Ser Gly Glu Asn Phe Pro Tyr Leu Val Ala 1575 1580 1585	5105
TAC CAA GCC ACC GTG TGC GCT AGG GCT CAA GCC CCT CCC CCA TCG TGG Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser Trp 1590 1595 1600	5153

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GAC CAG ATG CGG AAG TGT TTG ATC CGC CTT AAA CCC ACC CTC CAT GGG Asp Gln Met Arg Lys Cys Leu Ile Arg Leu Lys Pro Thr Leu His Gly 1605 1610 1615 1620	5201
CCA ACA CCC CTG CTA TAC AGA CTG GGC GCT GTT CAG AAT GAA GTC ACC Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn Glu Val Thr 1625 1630 1635	5249
CTG ACG CAC CCA ATC ACC AAA TAC ATC ATG ACA TGC ATG TCG GCC GAC Leu Thr His Pro Ile Thr Lys Tyr Ile Met Thr Cys Met Ser Ala Asp 1640 1645 1650	5297
CTG GAG GTC GTC ACG AGC ACC TGG GTG CTC GTT GGC GGC GTC CTG GCT Leu Glu Val Val Thr Ser Thr Trp Val Leu Val Gly Gly Val Leu Ala 1655 1660 1665	5345
GCT CTG GCC GCG TAT TGC CTG TCA ACA GGC TGC GTG GTC ATA GTG GGC Ala Leu Ala Ala Tyr Cys Leu Ser Thr Gly Cys Val Val Ile Val Gly 1670 1675 1680	5393
AGG ATC GTC TTG TCC GGG AAG CCG GCA ATT ATA CCT GAC AGG GAG GTT Arg Ile Val Leu Ser Gly Lys Pro Ala Ile Ile Pro Asp Arg Glu Val 1685 1690 1695 1700	5441
CTC TAC CAG GAG TTC GAT GAG ATG GAA GAG TGC TCT CAG CAC TTA CCG Leu Tyr Gln Glu Phe Asp Glu Met Glu Glu Cys Ser Gln His Leu Pro 1705 1710 1715	5489
TAC ATC GAG CAA GGG ATG ATG CTC GCT GAG CAG TTC AAG CAG AAG GCC Tyr Ile Glu Gln Gly Met Met Leu Ala Glu Gln Phe Lys Gln Lys Ala 1720 1725 1730	5537
CTC GGC CTC CTG CAG ACC GCG TCC CGC CAT GCA GAG GTT ATC ACC CCT Leu Gly Leu Leu Gln Thr Ala Ser Arg His Ala Glu Val Ile Thr Pro 1735 1740 1745	5585
GCT GTC CAG ACC AAC TGG CAG AAA CTC GAG GTC TTT TGG GCG AAG CAC Ala Val Gln Thr Asn Trp Gln Lys Leu Glu Val Phe Trp Ala Lys His 1750 1755 1760	5633
ATG TGG AAT TTC ATC AGT GGG ATA CAA TAC TTG GCG GGC CTG TCA ACG Met Trp Asn Phe Ile Ser Gly Ile Gln Tyr Leu Ala Gly Leu Ser Thr 1765 1770 1775 1780	5681
CTG CCT GGT AAC CCC GCC ATT GCT TCA TTG ATG GCT TTT ACA GCT GCC Leu Pro Gly Asn Pro Ala Ile Ala Ser Leu Met Ala Phe Thr Ala Ala 1785 1790 1795	5729
GTC ACC AGC CCA CTA ACC ACT GGC CAA ACC CTC CTC TTC AAC ATA TTG Val Thr Ser Pro Leu Thr Thr Gly Gln Thr Leu Leu Phe Asn Ile Leu 1800 1805 1810	5777

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GGG GGG TGG GTG GCT GCC CAG CTC GCC GCC CCC GGT GCC GCT ACC GCC Gly Gly Trp Val Ala Ala Gln Leu Ala Ala Pro Gly Ala Ala Thr Ala 1815 1820 1825	5825
TTT GTG GGC GCT GGC TTA GCT GGC GCC GCA CTC GAC AGC GTT GGA CTG Phe Val Gly Ala Gly Leu Ala Gly Ala Ala Leu Asp Ser Val Gly Leu 1830 1835 1840	5873
GGG AAG GTC CTC GTG GAC ATT CTT GCA GGC TAT GGC GCG GGC GTG GCG Gly Lys Val Leu Val Asp Ile Leu Ala Gly Tyr Gly Ala Gly Val Ala 1845 1850 1855 1860	5921
GGA GCT CTT GTG GCA TTC AAG ATC ATG AGC GGT GAG GTC CCC TCC ACG Gly Ala Leu Val Ala Phe Lys Ile Met Ser Gly Glu Val Pro Ser Thr 1865 1870 1875	5969
GAG GAC CTG GTC AAT CTG CTG CCC GCC ATC CTC TCA CCT GGA GCC CTT Glu Asp Leu Val Asn Leu Leu Pro Ala Ile Leu Ser Pro Gly Ala Leu 1880 1885 1890	6017
GCA GTC GGT GTG GTC TTT GCA TCA ATA CTG CGC CGG CGT GTT GGC CCG Ala Val Gly Val Val Phe Ala Ser Ile Leu Arg Arg Arg Val Gly Pro 1895 1900 1905	6065
GGC GAG GGG GCA GTG CAA TGG ATG AAC CGG CTA ATA GCC TTC GCC TCC Gly Glu Gly Ala Val Gln Trp Met Asn Arg Leu Ile Ala Phe Ala Ser 1910 1915 1920	6113
CGG GGG AAC CAT GTT TCC CCC ACA CAC TAC GTG CCG GAG AGC GAT GCA Arg Gly Asn His Val Ser Pro Thr His Tyr Val Pro Glu Ser Asp Ala 1925 1930 1935 1940	6161
GCC GCC CGC GTC ACT GCC ATA CTC AGC AGC CTC ACT GTA ACC CAG CTC Ala Ala Arg Val Thr Ala Ile Leu Ser Ser Leu Thr Val Thr Gln Leu 1945 1950 1955	6209
CTG AGG CGA CTG CAT CAG TGG ATA AGC TCG GAG TGT ACC ACT CCA TGC Leu Arg Arg Leu His Gln Trp Ile Ser Ser Glu Cys Thr Thr Pro Cys 1960 1965 1970	6257
TCC GGT TCC TGG CTA AGG GAC ATC TGG GAC TGG ATA TGC GAG GTG CTG Ser Gly Ser Trp Leu Arg Asp Ile Trp Asp Trp Ile Cys Glu Val Leu 1975 1980 1985	6305
AGC GAC TTT AAG ACC TGG CTG AAA GCC AAG CTC ATG CCA CAA CTG CCT Ser Asp Phe Lys Thr Trp Leu Lys Ala Lys Leu Met Pro Gln Leu Pro 1990 1995 2000	6353
GGG ATT CCC TTT GTG TCC TGC CAG CGC GGG TAT AGG GGG GTC TGG CGA Gly Ile Pro Phe Val Ser Cys Gln Arg Gly Tyr Arg Gly Val Trp Arg 2005 2010 2015 2020	6401

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GGA GAC GGC ATT ATG CAC ACT CGC TGC CAC TGT GGA GCT GAG ATC ACT Gly Asp Gly Ile Met His Thr Arg Cys His Cys Gly Ala Glu Ile Thr 2025 2030 2035	6449
GGA CAT GTC AAA AAC GGG ACG ATG AGG ATC GTC GGT CCT AGG ACC TGC Gly His Val Lys Asn Gly Thr Met Arg Ile Val Gly Pro Arg Thr Cys 2040 2045 2050	6497
AAG AAC ATG TGG AGT GGG ACG TTC TTC ATT AAT GCC TAC ACC ACG GGC Lys Asn Met Trp Ser Gly Thr Phe Phe Ile Asn Ala Tyr Thr Thr Gly 2055 2060 2065	6545
CCC TGT ACT CCC CTT CCT GCG CCG AAC TAT AAG TTC GCG CTG TGG AGG Pro Cys Thr Pro Leu Pro Ala Pro Asn Tyr Lys Phe Ala Leu Trp Arg 2070 2075 2080	6593
GTG TCT GCA GAG GAA TAC GTG GAG ATA AGG CGG GTG GGG GAC TTC CAC Val Ser Ala Glu Glu Tyr Val Glu Ile Arg Arg Val Gly Asp Phe His 2085 2090 2095 2100	6641
TAC GTA TCG GGC ATG ACT ACT GAC AAT CTC AAA TGC CCG TGC CAG ATC Tyr Val Ser Gly Met Thr Thr Asp Asn Leu Lys Cys Pro Cys Gln Ile 2105 2110 2115	6689
CCA TCG CCC GAA TTT TTC ACA GAA TTG GAC GGG GTG CGC CTA CAT AGG Pro Ser Pro Glu Phe Phe Thr Glu Leu Asp Gly Val Arg Leu His Arg 2120 2125 2130	6737
TTT GCG CCC CCT TGC AAG CCC TTG CTG CGG GAG GAG GTA TCT TTC AGA Phe Ala Pro Pro Cys Lys Pro Leu Leu Arg Glu Glu Val Ser Phe Arg 2135 2140 2145	6785
GTA GGA CTC CAC GAG TAC CCG GTG GGG TCG CAA TTA CCT TGC GAG CCC Val Gly Leu His Glu Tyr Pro Val Gly Ser Gln Leu Pro Cys Glu Pro 2150 2155 2160	6833
GAA CCG GAC GTA GCC GTG TTG ACG TCC ATG CTC ACT GAT CCC TCC CAT Glu Pro Asp Val Ala Val Leu Thr Ser Met Leu Thr Asp Pro Ser His 2165 2170 2175 2180	6881
ATA ACA GCA GAG GCG GCC GGG AGA AGG TTG GCG AGA GGG TCA CCC CCT Ile Thr Ala Glu Ala Ala Gly Arg Arg Leu Ala Arg Gly Ser Pro Pro 2185 2190 2195	6929
TCT ATG GCC AGC TCC TCG GCT AGC CAG CTG TCC GCT CCA TCT CTC AAG Ser Met Ala Ser Ser Ser Ala Ser Gln Leu Ser Ala Pro Ser Leu Lys 2200 2205 2210	6977
GCA ACT TGC ACC GCC AAC CAT GAC TCC CCT GAC GCC GAG CTC ATA GAG Ala Thr Cys Thr Ala Asn His Asp Ser Pro Asp Ala Glu Leu Ile Glu 2215 2220 2225	7025

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GCT AAC CTC CTG TGG AGG CAG GAG ATG GGC GGC AAC ATC ACC AGG GTT Ala Asn Leu Leu Trp Arg Gln Glu Met Gly Gly Asn Ile Thr Arg Val 2230 2235 2240	7073
GAG TCA GAG AAC AAA GTG GTG ATT CTG GAC TCC TTC GAT CCG CTT GTG Glu Ser Glu Asn Lys Val Val Ile Leu Asp Ser Phe Asp Pro Leu Val 2245 2250 2255 2260	7121
GCA GAG GAG GAT GAG CGG GAG GTC TCC GTA CCC GCA GAA ATT CTG CGG Ala Glu Glu Asp Glu Arg Glu Val Ser Val Pro Ala Glu Ile Leu Arg 2265 2270 2275	7169
AAG TCT CGG AGA TTC GCC CCA GCC CTG CCC GTC TGG GCG CGG CCG GAC Lys Ser Arg Arg Phe Ala Pro Ala Leu Pro Val Trp Ala Arg Pro Asp 2280 2285 2290	7217
TAC AAC CCC CTG CTA GTA GAG ACG TGG AAA AAG CCT GAC TAC GAA CCA Tyr Asn Pro Leu Leu Val Glu Thr Trp Lys Lys Pro Asp Tyr Glu Pro 2295 2300 2305	7265
CCT GTG GTC CAT GGC TGC CCG CTA CCA CCT CCA CGG TCC CCT CCT GTG Pro Val Val His Gly Cys Pro Leu Pro Pro Pro Arg Ser Pro Pro Val 2310 2315 2320	7313
CCT CCG CCT CGG AAA AAG CGT ACG GTG GTC CTC ACC GAA TCA ACC CTA Pro Pro Pro Arg Lys Lys Arg Thr Val Val Leu Thr Glu Ser Thr Leu 2325 2330 2335 2340	7361
CCT ACT GCC TTG GCC GAG CTT GCC ACC AAA AGT TTT GGC AGC TCC TCA Pro Thr Ala Leu Ala Glu Leu Ala Thr Lys Ser Phe Gly Ser Ser Ser 2345 2350 2355	7409
ACT TCC GGC ATT ACG GGC GAC AAT ACG ACA ACA TCC TCT GAG CCC GCC Thr Ser Gly Ile Thr Gly Asp Asn Thr Thr Thr Ser Ser Glu Pro Ala 2360 2365 2370	7457
CCT TCT GGC TGC CCC CCC GAC TCC GAC GTT GAG TCC TAT TCT TCC ATG Pro Ser Gly Cys Pro Pro Asp Ser Asp Val Glu Ser Tyr Ser Ser Met 2375 2380 2385	7505
CCC CCC CTG GAG GGG GAG CCT GGG GAT CCG GAT CTC AGC GAC GGG TCA Pro Pro Leu Glu Gly Glu Pro Gly Asp Pro Asp Leu Ser Asp Gly Ser 2390 2395 2400	7553
TGG TCG ACG GTC AGT AGT GGG GCC GAC ACG GAA GAT GTC GTG TGC TGC Trp Ser Thr Val Ser Ser Gly Ala Asp Thr Glu Asp Val Val Cys Cys 2405 2410 2415 2420	7601
TCA ATG TCT TAT TCC TGG ACA GGC GCA CTC GTC ACC CCG TGC GCT GCG Ser Met Ser Tyr Ser Trp Thr Gly Ala Leu Val Thr Pro Cys Ala Ala 2425 2430 2435	7649

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GAG GAA CAA AAA CTG CCC ATC AAC GCA CTG AGC AAC TCG TTG CTA CGC Glu Glu Gln Lys Leu Pro Ile Asn Ala Leu Ser Asn Ser Leu Leu Arg 2440 2445 2450	7697
CAT CAC AAT CTG GTG TAT TCC ACC ACT TCA CGC AGT GCT TGC CAA AGG His His Asn Leu Val Tyr Ser Thr Thr Ser Arg Ser Ala Cys Gln Arg 2455 2460 2465	7745
AAG AAG AAA GTC ACA TTT GAC AGA CTG CAA GTT CTG GAC AGC CAT TAC Lys Lys Lys Val Thr Phe Asp Arg Leu Gln Val Leu Asp Ser His Tyr 2470 2475 2480	7793
CAG GAC GTG CTC AAG GAG GTC AAA GCA GCG GCG TCA AAA GTG AAG GCT Gln Asp Val Leu Lys Glu Val Lys Ala Ala Ala Ser Lys Val Lys Ala 2485 2490 2495 2500	7841
AAC TTG CTA TCC GTA GAG GAA GCT TGC AGC CTG GCG CCC CCA CAT TCA Asn Leu Leu Ser Val Glu Glu Ala Cys Ser Leu Ala Pro Pro His Ser 2505 2510 2515	7889
GCC AAA TCC AAG TTT GGC TAT GGG GCA AAA GAC GTC CGT TGC CAT GCC Ala Lys Ser Lys Phe Gly Tyr Gly Ala Lys Asp Val Arg Cys His Ala 2520 2525 2530	7937
AGA AAG GCC GTA GCC CAC ATC AAC TCC GTG TGG AAA GAC CTT CTG GAA Arg Lys Ala Val Ala His Ile Asn Ser Val Trp Lys Asp Leu Leu Glu 2535 2540 2545	7985
GAC AGT GTA ACA CCA ATA GAC ACT ACC ATC ATG GCC AAG AAC GAG GTT Asp Ser Val Thr Pro Ile Asp Thr Thr Ile Met Ala Lys Asn Glu Val 2550 2555 2560	8033
TTC TGC GTT CAG CCT GAG AAG GGG GGT CGT AAG CCA GCT CGT CTC ATC Phe Cys Val Gln Pro Glu Lys Gly Gly Arg Lys Pro Ala Arg Leu Ile 2565 2570 2575 2580	8081
GTG TTC CCC GAC CTG GGC GTG CGC GTG TGC GAG AAG ATG GCC CTG TAC Val Phe Pro Asp Leu Gly Val Arg Val Cys Glu Lys Met Ala Leu Tyr 2585 2590 2595	8129
GAC GTG GTT AGC AAG CTC CCC TTG GCC GTG ATG GGA AGC TCC TAC GGA Asp Val Val Ser Lys Leu Pro Leu Ala Val Met Gly Ser Ser Tyr Gly 2600 2605 2610	8177
TTC CAA TAC TCA CCA GGA CAG CGG GTT GAA TTC CTC GTG CAA GCG TGG Phe Gln Tyr Ser Pro Gly Gln Arg Val Glu Phe Leu Val Gln Ala Trp 2615 2620 2625	8225
AAG TCC AAG AAG ACC CCG ATG GGG CTC TCG TAT GAT ACC CGC TGT TTT Lys Ser Lys Lys Thr Pro Met Gly Leu Ser Tyr Asp Thr Arg Cys Phe 2630 2635 2640	8273

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GAC TCC ACA GTC ACT GAG AGC GAC ATC CGT ACG GAG GAG GCA ATT TAC Asp Ser Thr Val Thr Glu Ser Asp Ile Arg Thr Glu Glu Ala Ile Tyr 2645 2650 2655 2660	8321
CAA TGT TGT GAC CTG GAC CCC CAA GCC CGC GTG GCC ATC AAG TCC CTC Gln Cys Cys Asp Leu Asp Pro Gln Ala Arg Val Ala Ile Lys Ser Leu 2665 2670 2675	8369
ACT GAG AGG CTT TAT GTT GGG GGC CCT CTT ACT AAT TCA AGG GGG GAA Thr Glu Arg Leu Tyr Val Gly Gly Pro Leu Thr Asn Ser Arg Gly Glu 2680 2685 2690	8417
AAC TGC GGC TAC CGC AGG TGC CGC GCG AGC AGA GTA CTG ACA ACT AGC Asn Cys Gly Tyr Arg Arg Cys Arg Ala Ser Arg Val Leu Thr Thr Ser 2695 2700 2705	8465
TGT GGT AAC ACC CTC ACT CGC TAC ATC AAG GCC CGG GCA GCC TGT CGA Cys Gly Asn Thr Leu Thr Arg Tyr Ile Lys Ala Arg Ala Ala Cys Arg 2710 2715 2720	8513
GCC GCA GGG CTC CAG GAC TGC ACC ATG CTC GTG TGT GGC GAC GAC TTA Ala Ala Gly Leu Gln Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu 2725 2730 2735 2740	8561
GTC GTT ATC TGT GAA AGT GCG GGG GTC CAG GAG GAC GCG GCG AGC CTG Val Val Ile Cys Glu Ser Ala Gly Val Gln Glu Asp Ala Ala Ser Leu 2745 2750 2755	8609
AGA GCC TTC ACG GAG GCT ATG ACC AGG TAC TCC GCC CCC CCC GGG GAC Arg Ala Phe Thr Glu Ala Met Thr Arg Tyr Ser Ala Pro Pro Gly Asp 2760 2765 2770	8657
CCC CCA CAA CCA GAA TAC GAC TTG GAG CTT ATA ACA TCA TGC TCC TCC Pro Pro Gln Pro Glu Tyr Asp Leu Glu Leu Ile Thr Ser Cys Ser Ser 2775 2780 2785	8705
AAC GTG TCA GTC GCC CAC GAC GGC GCT GGA AAG AGG GTC TAC TAC CTT Asn Val Ser Val Ala His Asp Gly Ala Gly Lys Arg Val Tyr Tyr Leu 2790 2795 2800	8753
ACC CGT GAC CCT ACA ACC CCC CTC GCG AGA GCC GCG TGG GAG ACA GCA Thr Arg Asp Pro Thr Thr Pro Leu Ala Arg Ala Ala Trp Glu Thr Ala 2805 2810 2815 2820	8801
AGA CAC ACT CCA GTC AAT TCC TGG CTA GGC AAC ATA ATC ATG TTT GCC Arg His Thr Pro Val Asn Ser Trp Leu Gly Asn Ile Ile Met Phe Ala 2825 2830 2835	8849
CCC ACA CTG TGG GCG AGG ATG ATA CTG ATG ACC CAC TTC TTT AGC GTC Pro Thr Leu Trp Ala Arg Met Ile Leu Met Thr His Phe Phe Ser Val 2840 2845 2850	8897

CTC ATA GCC AGG GAT CAG CTT GAA CAG GCT CTC AAC TGC GAG ATC TAC Leu Ile Ala Arg Asp Gln Leu Glu Gln Ala Leu Asn Cys Glu Ile Tyr 2855 2860 2865	8945
GGA GCC TGC TAC TCC ATA GAA CCA CTG GAT CTA CCT CCA ATC ATT CAA Gly Ala Cys Tyr Ser Ile Glu Pro Leu Asp Leu Pro Pro Ile Ile Gln 2870 2875 2880	8993
AGA CTC CAT GGC CTC AGC GCA TTT TCA CTC CAC AGT TAC TCT CCA GGT Arg Leu His Gly Leu Ser Ala Phe Ser Leu His Ser Tyr Ser Pro Gly 2885 2890 2895 2900	9041
GAA ATT AAT AGG GTG GCC GCA TGC CTC AGA AAA CTT GGG GTC CCG CCC Glu Ile Asn Arg Val Ala Ala Cys Leu Arg Lys Leu Gly Val Pro Pro 2905 2910 2915	9089
TTG CGA GCT TGG AGA CAC CGG GCC TGG AGC GTC CGC GCT AGG CTT CTG Leu Arg Ala Trp Arg His Arg Ala Trp Ser Val Arg Ala Arg Leu Leu 2920 2925 2930	9137
GCC AGA GGA GGC AAG GCT GCC ATA TGT GGC AAG TAC CTC TTC AAC TGG Ala Arg Gly Gly Lys Ala Ala Ile Cys Gly Lys Tyr Leu Phe Asn Trp 2935 2940 2945	9185
GCA GTA AGA ACA AAG CTC AAA CTC ACT CCG ATA ACG GCC GCT GGC CGG Ala Val Arg Thr Lys Leu Lys Leu Thr Pro Ile Thr Ala Ala Gly Arg 2950 2955 2960	9233
CTG GAC TTG TCC GGC TGG TTC ACG GCT GGC TAC AGC GGG GGA GAC ATT Leu Asp Leu Ser Gly Trp Phe Thr Ala Gly Tyr Ser Gly Gly Asp Ile 2965 2970 2975 2980	9281
TAT CAC AGC GTG TCT CAT GCC CGG CCC CGC TGG TTC TGG TTT TGC CTA Tyr His Ser Val Ser His Ala Arg Pro Arg Trp Phe Trp Phe Cys Leu 2985 2990 2995	9329
CTC CTG CTT GCT GCA GGG GTA GGC ATC TAC CTC CTC CCC AAC CGA Leu Leu Leu Ala Ala Gly Val Gly Ile Tyr Leu Leu Pro Asn Arg 3000 3005 3010	9374
TGAAGATTGG GCTAACCACT CCAGGCCAAT AGGCCATTCC CT	9416

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

174

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CAGCCCCCTG ATGGGGGCGA C

21

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

ACTCGCAAGC ACCCTATCA

19

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CTGTGAGGAA CTACTGTCT

19

(2) INFORMATION FOR SEQ ID NO:50:

175

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

ATGAGCACGA ATCCTCAAAC CT

22

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GTCCTGCCCT CGGGCC

16

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CGAGGAAGAC TTCCGAGC

18

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

ACCCAAATTG CGCGACCTAC

20

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

TAAGGTCATC GATACCCT

18

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid

177

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CAGTTCATCA TCATATCCCA

20

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

AGATAGAGAA AGAGCAAC

18

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

178

AGACTTCCGA GCGGTCGCAA

20

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GACCTGTGCG GGTCTGTC

18

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GGGTCGGCAG CTGGCTAGCC TCTCA

25

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

179

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

TCCTGGCGGG CATAGCGT

18

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CCCCAGCCCT GGTCAAATC GGTA

25

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

180

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

CTGTCGGTCG TTCCACCA

19

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

CCGCGAAGAG TGTGTGTGGT

20

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

181

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

CAATGTTCTG GTGGAGGTG

19

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GCCATTAAGT GGGAGTACGT CGTTCTCC

28

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CGAGGAAGGA TACAAGACC

19

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid

182

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

TGCTTGTTGGA TGATGCTACT

20

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CACACGTGCA GTTGCCT

18

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

183

CTGCTGACCA CTACACAG

18

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GACCAGAGTG GAAGCGCAA

19

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TACCAGAGTC GGGTGTACAG

20

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

184

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

CTAGGAGGCC CCTTGTCTGC

20

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

CTCGGGCCAG CCGATGGA

18

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

GGGGACCTCA TGGTTGTCT

19

(2) INFORMATION FOR SEQ ID NO:76:

185

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

CCCGTGGAGT GGCTAAGG

18

- (2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: YES

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

CTCCTCGATG TTGGGATGG

19

- (2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CAGAGCTTCC AGGTGGCTC

19

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

CGGGCTCCGT CACTGTG

17

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GTATTGCAGT CTATCACCGA G

21

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid

187

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

GGCTATACCG GCGACTTCGA

20

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

CGTTGAGTGC GGGAGACAG

19

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

188

TCACCATTGA GACAATCACG

20

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GTAAGGAAGG TTCTCCCCAC TC

22

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

ATGCCCACTT TCTATCCCAG ACAAAGC

27

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

189

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

TGCATGTCAT GATGTAT

17

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GGACAAGACG ACCCTGCC

18

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CGTATTGCCT GTCAACAGGC

20

(2) INFORMATION FOR SEQ ID NO:89:

190

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: YES

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

AGCGCCCACA AAGGCAGTAG

20

- (2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CCTCTTCAAC ATATTGGGG

19

- (2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: YES

191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

CCAGGAACCG GAGCATGG

18

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

ACCAGTGGAT AAGCTCGG

18

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

CGTGGTGTAG GCATTAATG

19

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid

192

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ATGTGGAGTG GGACCTTCC

19

- (2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: YES

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

CTCTGCTGTT ATATGGGAGG

20

- (2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

193

GTTGACGTCC ATGCTCACTG

20

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

TTTCCACGTC TCCACTAGCG

20

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GTGAGGACCA CCGTCCGC

18

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

194

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

TTCCACCTCC AAAGTCCCCT

20

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

AGAACTTGCA GTCTGTCAAA TGTGA

25

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GGAAGAACAG AACTGCCCA TCAATGCACT AAGC

34

(2) INFORMATION FOR SEQ ID NO:102:

195

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

TGACGCCGCT GCTTTAACCT

20

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

TGCAAGCTTC CTCTACGGAT

20

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

196

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

AGGTTAAAGC AGCGGCGTCA

20

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

AGCTTCCCAT CACGGCCAA

19

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GATGGCTTTG TACGACGTG

19

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid

197

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

GCACCTGCGA TAGCCGCACT

20

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GTCCCTCACC GAGAGGCT

18

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GATTGGAGGT AGATCAAGTG

20

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

TACGACTTGG AGCTCATAAC

20

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

AGCAAGACAC ACTCCAGTCA

20

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

GCCTATTGGC CTGGAGTGGT TAGC

24

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

His	Val	Thr	Gly	Gly	Asn	Ala	Gly	Arg	Thr	Thr	Ala	Gly	Leu	Val	Gly
1			5					10					15		

Leu	Leu	Thr	Pro	Gly	Ala	Lys	Gln	Asn	Ile
		20					25		

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

His	Val	Thr	Gly	Gly	Ser	Ala	Gly	His	Thr	Val	Ser	Gly	Phe	Val	Ser
1			5					10					15		

Leu	Leu	Ala	Pro	Gly	Ala	Lys	Gln	Asn	Val
		20					25		

(2) INFORMATION FOR SEQ ID NO:115:

200

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

His	Val	Thr	Gly	Gly	Gln	Ala	Ala	Arg	Ala	Met	Ser	Gly	Leu	Val	Ser
1				5				10						15	
Leu	Phe	Thr	Pro	Gly	Ala	Lys	Gln	Asn	Ile						
			20					25							

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

His	Val	Thr	Gly	Gly	Arg	Val	Ala	Ser	Ser	Thr	Gln	Ser	Leu	Val	Ser
1				5				10						15	
Trp	Leu	Ser	Gln	Gly	Pro	Ser	Gln	Lys	Ile						
			20					25							

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

His	Val	Thr	Gly	Gly	Ala	Gln	Ala	Lys	Thr	Thr	Asn	Arg	Leu	Val	Ser
1				5				10						15	

201

Met Phe Ala Ser Gly Pro Ser Gln Lys Ile
 20 25

(2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Tyr Thr Ser Gly Gly Ala Ala Ser His Thr Thr Ser Thr Leu Ala Ser
 1 5 10 15

Leu Phe Ser Pro Gly Ala Ser Arg Asn Ile
 20 25

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

His Val Thr Gly Gly Val Gln Gly His Val Thr Ser Thr Leu Thr Ser
 1 5 10 15

Leu Phe Arg Pro Gly Ala Ser Gln Lys Ile
 20 25

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

His	Val	Thr	Gly	Gly	Ser	Ala	Gly	Arg	Thr	Thr	Ala	Gly	Leu	Val	Gly
1				5					10					15	
Leu	Leu	Thr	Pro	Gly	Ala	Lys	Gln	Asn	Ile						
			20					25							

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

His	Val	Thr	Gly	Gly	Ser	Ala	Gly	Arg	Ser	Val	Leu	Gly	Ile	Ala	Ser
1				5					10					15	
Phe	Leu	Thr	Arg	Gly	Pro	Lys	Gln	Asn	Ile						
			20					25							

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Val	Ala	Thr	Arg	Asp	Gly	Lys	Leu	Pro	Thr	Thr	Gln	Leu	Arg	Arg	His
1				5					10					15	
Ile	Asp	Leu	Leu	Val	Gly	Ser	Ala	Thr	Leu	Cys	Ser	Ala	Leu		
			20					25					30		

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Val Ala Thr Arg Asp Gly Lys Leu Pro Ala Thr Gln Leu Arg Arg His
1 5 10 15

Ile Asp Leu Leu Val Gly Ser Ala Thr Leu Cys Ser Ala Leu
20 25 30

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Leu Ala Ala Arg Asn Ser Ser Ile Pro Thr Thr Thr Ile Arg Arg His
1 5 10 15

Val Asp Leu Leu Val Gly Ala Ala Ala Leu Cys Ser Ala Met
20 25 30

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Leu Ala Ala Arg Asn Val Thr Ile Pro Thr Thr Thr Ile Arg Arg His
1 5 10 15

Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys Ser Ala Met
20 25 30

(2) INFORMATION FOR SEQ ID NO:126:

204

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Leu	Ala	Ala	Arg	Asn	Ala	Ser	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His
1				5					10					15	
Val	Asp	Leu	Leu	Val	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met		
		20						25					30		

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Leu	Ala	Ala	Arg	Asn	Ala	Ser	Val	Pro	Thr	Thr	Thr	Leu	Arg	Arg	His
1				5					10					15	
Val	Asp	Leu	Leu	Val	Gly	Thr	Ala	Ala	Phe	Cys	Ser	Ala	Met		
		20						25					30		

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Leu	Ala	Ser	Cys	Arg	Arg	Leu	Thr	Asp	Phe	Ala	Gln	Gly	Trp	Gly	Pro
1				5					10					15	

205

Ile Ser Tyr Ala Asn Gly Ser Gly Leu Asp Glu
20 25

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Leu Ala Ser Cys Arg Pro Leu Thr Asp Phe Asp Gln Gly Trp Gly Pro
1 5 10 15

Ile Ser Tyr Ala Asn Gly Ser Gly Pro Asp Gln
20 25

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Leu Ala Ser Cys Arg Arg Leu Thr Asp Phe Asp Gln Gly Trp Gly Pro
1 5 10 15

Ile Ser His Ala Asn Gly Ser Gly Pro Asp Gln
20 25

(2) INFORMATION FOR SEQ ID NO:131:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

Met Ala Ser Cys Arg Pro Ile Asp Glu Phe Ala Gln Gly Trp Gly Pro
1 5 10 15
Ile Thr His Asp Met Pro Glu Ser Ser Asp Gln
20 25

(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Met Ala Gln Cys Arg Thr Ile Asp Lys Phe Asp Gln Gly Trp Gly Pro
1 5 10 15
Ile Thr Tyr Ala Glu Ser Ser Arg Ser Asp Gln
20 25

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

Met Ala Ser Cys Arg Pro Ile Gln Trp Phe Ala Gln Gly Trp Gly Pro
1 5 10 15
Ile Thr Tyr Thr Glu Pro Asp Ser Pro Asp Gln
20 25

(2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
(B) TYPE: amino acid

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Leu	Ala	Ser	Cys	Arg	Arg	Leu	Thr	Asp	Phe	Asp	Gln	Gly	Trp	Gly	Pro
1				5					10					15	

Ile	Ser	Tyr	Ala	Asn	Gly	Ser	Gly	Pro	Asp	Glu
			20					25		

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Ser	Thr	Ser	Gly	Ile	Thr	Gly	Asp	Asn	Thr	Thr	Thr	Ser	Ser	Glu	Pro
1				5					10					15	

Ala	Pro	Ser	Gly	Cys	Pro	Pro	Asp
			20				

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Gly	Ser	Ser	Ala	Val	Asp	Ser	Gly	Thr	Ala	Thr	Gly	Pro	Pro	Asp	Gln
1				5					10					15	

Ala	Ser	Asp	Asp	Gly	Asp	Lys	Gly
				20			

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(2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

Glu	Ser	Ser	Ala	Val	Asp	Ser	Gly	Thr	Ala	Thr	Ala	Leu	Pro	Asp	Gln
1				5				10						15	

Ala	Ser	Asp	Asp	Gly	Asp	Lys	Gly
				20			

What Is Claimed Is:

1. A DNA sequence encoding the genome of a non-A, non-B hepatitis virus (NANBV) belonging to the Hutch subgroup, said DNA sequence being selected from the group of the following DNA sequences:

5 (a) the Hutch c59 DNA sequence shown in SEQ ID NO:46;

(b) a DNA sequence encoding the same polyprotein as the DNA sequence (a) but which differs from said DNA sequence (a) as a result of the degeneration of the genetic code;

10 (c) a DNA sequence which hybridizes to said DNA sequence (a) or (b) and represents a mutant or variant of the NANBV Hutch c59 strain displaying essentially the same specific immunological properties; and

15 (d) a DNA sequence which hybridizes to said DNA sequence (a) or (b) and represents a NANBV strain having the immunological properties of the Hutch subgroup.

20 2. A DNA sequence having a length of about 10 to 200 nucleotides that corresponds to a portion of the DNA sequence of claim 1, said DNA sequence having at least one nucleotide difference in sequence when compared to the nucleotide sequence of a strain of NANBV selected from the group consisting of HCV-1, HCV-BK, HCV-J, HC-J1, HC-J4, HCV-JH and HCV-Hh, wherein said nucleotide difference represents a silent mutation or a mutation causing a difference in at least one amino acid.

30 3. A DNA sequence encoding a variable region of the NANBV genome or a portion thereof, said region or portion thereof having an amino acid sequence, the SEQ

35

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ID NO and corresponding residues of which are shown in parenthesis, selected from the group consisting of:

(a) the V variable region:

-HVTGGNAGRTTAGLVGLLTPGAKQNI-

5

(46 : 386-411);

(b) a part of V:

-NAGRTTAGLVGLLT-

(46 : 391-404);

(c) the V_1 variable region:

10

-VATRDGKLPTTQLRRHIDLLVGSATL

GSAL- (46 : 246-275);

(d) a part of V_1 :

-VATRDGKLPTT-

(46 : 246-256);

15

(e) the V_2 variable region:

-LASCRRRLTDFAGWGPISYANGSGLDE-

(46 : 456-482);

(f) a part of V_2 :

-RLTDFA-

20

(46 : 461-466)

(g) a part of V_2 :

-SYANGSGLDE-

(46 : 473-482); and

(h) the V_3 variable region

25

-STSGITGDNTTTSSEPAPSGCPPD-

(46 : 2356-2379).

4. A DNA sequence derived from a NANBV genome and encoding a variable region or a portion thereof corresponding to the variable region or portion thereof encoded by any of the DNA sequences characterized in claim 3.

30

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5. A DNA sequence having a length of about 18 to 200 nucleotides comprising a DNA sequence of claim 3 or 4.

5 6. A DNA sequence according to claim 3 or 5 corresponding to a sequence shown in SEQ ID NO:46.

10 7. A DNA sequence that encodes the NANBV structural capsid protein having an amino acid sequence contained in SEQ ID NO:1 from residue 1 to 120 or that encodes an immunologically active part of said protein.

15 8. A DNA sequence that hybridizes to the DNA sequence of claim 7 and that encodes a NANBV structural capsid protein or an immunologically active part thereof.

20 9. A DNA sequence encoding a part of the NANBV structural capsid protein having an amino acid sequence contained in SEQ ID NO:1 from residue 1 to residue 20.

25 10. A DNA sequence encoding a part of the NANBV structural capsid protein having an amino acid sequence contained in SEQ ID NO:1 from residue 1 to residue 74.

30 11. A DNA sequence encoding a part of the NANBV structural capsid protein having an amino acid sequence contained in SEQ ID NO:1 from residue 21 to residue 40.

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12. A DNA sequence encoding a part of the NANBV structural capsid protein having an amino acid sequence contained in SEQ ID NO:1 from residue 2 to residue 40.

5

13. A DNA sequence encoding a part of the NANBV structural capsid protein having an amino acid sequence contained in SEQ ID NO:1 from residue 69 to residue 120.

10

14. A DNA sequence encoding a part of the NANBV structural capsid protein having an amino acid sequence contained in SEQ ID NO:1 from residue 121 to residue 326 or that encodes an immunologically active part of said protein.

15

15. A DNA sequence that hybridizes to the DNA sequence of claim 14 and that encodes a NANBV structural envelope protein or an immunologically active part thereof.

20

16. A DNA sequence encoding a part of the NANBV structural envelope protein having an amino acid sequence contained in SEQ ID NO:1 from residue 121 to residue 176.

25

17. A DNA sequence that encodes the amino acid sequence contained in SEQ ID NO:1 from residue 1 to residue 326 or that encodes an immunologically active part of said amino acid sequence.

30

18. A DNA sequence comprising a DNA sequence of any one of claims 1 to 17.

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19. A recombinant DNA molecule comprising a vector operatively linked to a DNA sequence according to any one of claims 1 to 18.

5 20. The recombinant DNA molecule of claim 19 wherein said vector is an expression vector, said molecule is capable of expressing said protein in a compatible host, and said NANBV structural protein has an amino acid residue sequence shown in SEQ ID NO:2
10 from residue 1 to residue 315.

 21. The recombinant DNA molecule of claim 19 wherein said vector is an expression vector, said molecule is capable of expressing said protein in a
15 compatible host, and said NANBV structural protein has an amino acid residue sequence contained in SEQ ID NO:3 from residue 1 to residue 252.

 22. The recombinant DNA molecule of claim 19 wherein said vector is an expression vector, said
20 molecule is capable of expressing said protein in a compatible host, and said NANBV structural protein has an amino acid residue sequence contained in SEQ ID NO:4 from residue 1 to residue 252.

25 23. The recombinant DNA molecule of claim 19 wherein said vector is an expression vector and said molecule is capable of expressing said protein in a compatible host, and said NANBV structural protein has
30 an amino acid residue sequence contained in SEQ ID NO:6 from residue 1 to residue 271.

 24. A transformed host cell containing a DNA sequence of any one of claims 1 to 18 or a recombinant
35 DNA molecule according to any one of claims 19 to 23.

25. A polypeptide or peptide encoded by a DNA sequence of any one of claims 1 to 18 or a recombinant DNA molecule of any one of claims 19 to 23.

5 26. The polypeptide or peptide of claim 25 having a length from about 7 to about 200 amino acid residues.

10 27. The polypeptide or peptide of claim 25 which is a NANBV structural protein having a length of at least 20 amino acids.

15 28. A composition comprising at least one polypeptide or peptide according to any one of claims 25 to 27.

20 29. An antibody that immunoreacts with a polypeptide or peptide according to any one of claims 25 to 27, but does not immunoreact with NANBV isolates HCV-1, HCV-BK, HCV-J, HC-J1, HC-J4, HCV-JH or HCV-Hh.

25 30. An antibody that immunoreacts with the Hutch c59 isolate of NANBV or a part thereof, but does not immunoreact with NANBV isolates HCV-1, HCV-BK, HCV-J, HC-J1, HC-J4, HCV-JH or HCV-Hh.

30 31. A diagnostic kit for assaying a body fluid sample for the presence of antibodies against NANBV structural antigens comprising, in an amount sufficient to perform at least one assay, at least one polypeptide or peptide according to any one of claims 25 to 27.

32. The diagnostic kit according to claim 31 wherein said polypeptide or peptide is affixed to a solid matrix.

- 5 33. A diagnostic kit for assaying a body fluid sample for the presence of NANBV structural antigens comprising, in an amount sufficient to perform at least one assay, an anti-NANBV structural protein antibody that:
- 10 (i) immunoreacts with (a) the Hutch c59 isolate of NANBV, (b) a polypeptide or peptide according to any one of claims 25 to 27;
- (ii) but does not immunoreact with (c) NANBV isolates HCV-1, HCV-BK, HCV-J, HC-J1, HC-J4, HCV-JH or
- 15 HCV-Hh, or (d) the C-100 antigen.

34. The diagnostic kit of claim 33 wherein said antibody is affixed to a solid matrix.

- 20 35. A method of assaying a body fluid sample for the presence of antibodies against a NANBV structural antigen, which method comprises:
- (a) forming an aqueous immunoreaction admixture by admixing said body sample with a
- 25 polypeptide or peptide of any one of claims 25 to 27;
- (b) maintaining said aqueous immunoreaction admixture for a time period sufficient for any of said antibodies present to immunoreact with said
- polypeptide or peptide to form an immunoreaction
- 30 product; and
- (c) detecting the presence of any of said immunoreaction product formed and thereby the presence of said antibodies.

36. The method of claim 35 wherein said polypeptide or peptide is affixed to a solid matrix.

37. The method of claim 36 wherein said detecting in step (c) comprises the steps of:

(i) admixing said immunoreaction product formed in step (c) with a labeled specific binding agent to form a labeling admixture, said labeled specific binding agent comprising a specific binding agent and a label;

(ii) maintaining said labeling admixture for a period sufficient for any of said immunoreaction product present to bind with said labeled specific binding agent to form a labeled product; and

(iii) detecting the presence of any of said labeled product formed, and thereby the presence of said immunoreaction product.

38. The method of claim 37 wherein said specific binding agent is selected from the group consisting of Protein A and at least one of the antibodies anti-human IgG and anti-human IgM.

39. The method of claim 37 wherein said label is selected from the group consisting of lanthanide chelate, biotin, enzyme and radioactive isotope.

40. A method of assaying a body sample for the presence of NANBV polynucleic acids which method comprises:

(a) forming an aqueous hybridization admixture by admixing said body sample with a polynucleotide or oligonucleotide having a DNA sequence according to any one of claims 1 to 18;

(b) maintaining said aqueous hybridization admixture for a time period and under hybridizing conditions sufficient for any of said NANBV polynucleic acids present to hybridize with said polynucleotide or oligonucleotide to form a hybridization product; and

(c) detecting the presence of any of said hybridization product formed and thereby the presence of said NANBV polynucleic acids.

41. A method of assaying a body fluid sample for the presence of NANBV structural antigens, which method comprises reacting said sample with an antibody according to claim 29 or 30.

42. An inoculum comprising an immunologically effective amount of a polypeptide or peptide according to any one of claims 25 to 27, said polypeptide or peptide being either alone or linked to an antigenic carrier and dispersed in a pharmaceutically acceptable excipient.

43. A vaccine comprising an immunologically effective amount of a polypeptide or peptide according to any one of claims 25 to 27, said polypeptide or peptide being either alone or linked to an antigenic carrier and dispersed in a pharmaceutically acceptable excipient.

44. A method of producing a NANBV structural protein comprising:

(a) initiating a culture comprising a nutrient medium containing transformed host cells according to claim 24;

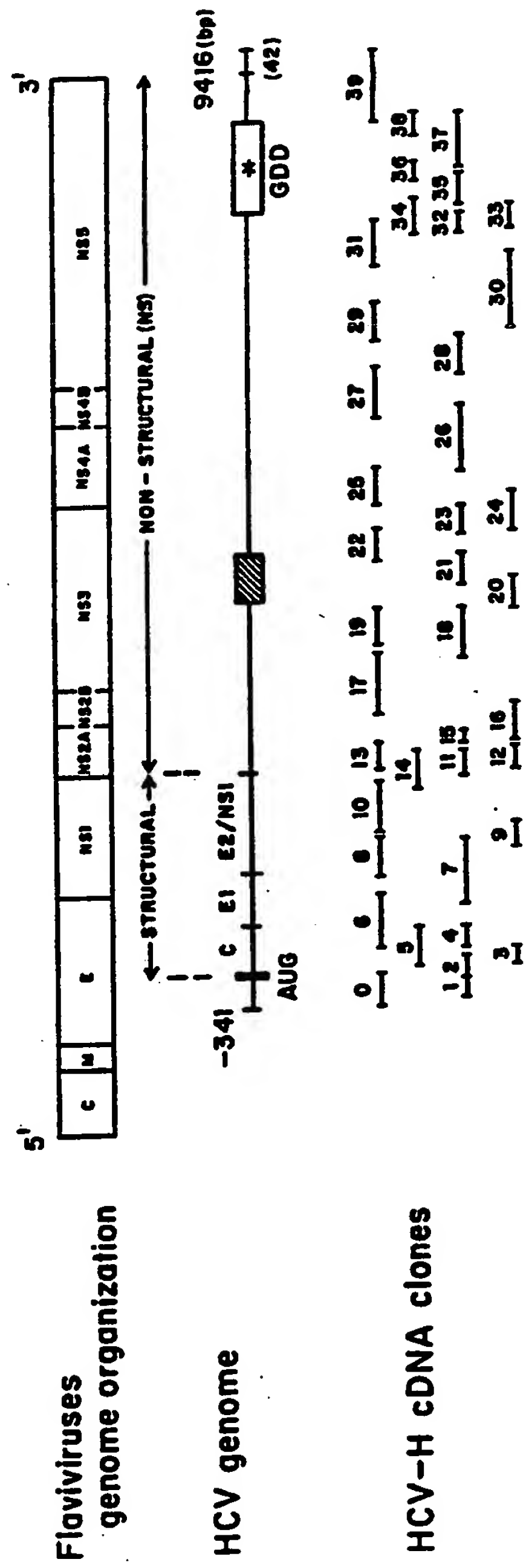
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(b) maintaining the culture for a time period sufficient for the transformed host cells to express NANBV structural protein; and

5 (c) recovering the NANBV structural protein from the culture.

45. A method for inducing antibody production in a mammal, said antibody being immunoreactive with NANBV, comprising (a) administering an inoculum
10 according to claim 42 or a vaccine according to claim 43 to said mammal, and (b) maintaining the mammal for a time period sufficient for said mammal to respond immunologically and produce anti-NANBV antibody.

15



 = NS3 dengue type 2
 = replicase CARMV

FIGURE 1

INTERNATIONAL SEARCH REPORT

International Application No. PCT/US91/06037

I. CLASSIFICATION OF SUBJECT MATTER (if several classification symbols apply, indicate all) * According to International Patent Classification (IPC) or to both National Classification and IPC U.S. CL.: 536/27; 530/350, 387; 435/5; 424/89 IPC(5): C07H 15/12; C07K 3/00; C12Q 1/70; A61K 39/12		
II. FIELDS SEARCHED Minimum Documentation Searched 7		
Classification System	Classification Symbols	
U.S.	536/27; 530/350, 387; 435/5; 424/89	
Documentation Searched other than Minimum Documentation to the extent that such Documents are included in the Fields Searched 8		
STIC Sequence Search APS		
III. DOCUMENTS CONSIDERED TO BE RELEVANT 9		
Category *	Citation of Document, 11 with indication, where appropriate, of the relevant passages 12	Relevant to Claim No. 13
Y	Gene. Volume 91, issued 1990, K. Takeuchi et al.. "Hepatitis C viral cDNA isolated from a healthy carrier donor implicated in post-transfusion non-A, non-B hepatitis," pages 287-291, see entire document.	1,3-6
$\frac{N}{Y}$	EP. A. 0.318,216 (Houghton et al.) 31 May 1989. see figures and claims.	$\frac{16}{3-15,17-45}$
$\frac{N}{Y}, P$	EP. A. 0,388,232 (Houghton et al.) 19 September 1990. see figures and claims.	$\frac{16}{1-15,17-45}$
* Special categories of cited documents: 10 "A" document defining the general state of the art which is not considered to be of particular relevance "E" earlier document but published on or after the international filing date "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) "O" document referring to an oral disclosure, use, exhibition or other means "P" document published prior to the international filing date but later than the priority date claimed "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such docu- ments, such combination being obvious to a person skilled in the art. "A" document member of the same patent family		
IV. CERTIFICATION		
Date of the Actual Completion of the International Search 07 January 1992		Date of Mailing of this International Search Report 24 JAN 1992
International Searching Authority ISA/US		Signature of Authorized Officer Donna C. Wortman

FURTHER INFORMATION CONTINUED FROM THE SECOND SHEET

V. ☐ OBSERVATIONS WHERE CERTAIN CLAIMS WERE FOUND UNSEARCHABLE ¹

This international search report has not been established in respect of certain claims under Article 17(2) (a) for the following reasons:

1. ☐ Claim numbers _____, because they relate to subject matter ¹² not required to be searched by this Authority, namely:

2. ☐ Claim numbers _____, because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out ¹³, specifically:

3. ☐ Claim numbers _____, because they are dependent claims not drafted in accordance with the second and third sentences of PCT Rule 6.4(a).

VI. ☒ OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING ²

This International Searching Authority found multiple inventions in this international application as follows:

See attached sheet.

1. ☒ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims of the international application. **telephone practice**
2. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims of the international application for which fees were paid, specifically claims:
3. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claim numbers:
4. ☐ As all searchable claims could be searched without effort justifying an additional fee, the International Searching Authority did not invite payment of any additional fee.

Remark on Protest

- ☐ The additional search fees were accompanied by applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

Attachment to PCT/IPEA/210

VI. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING

Group I, Claims 1-24 and 40, drawn to DNA sequences, recombinant DNA, transformed host cell, and first method of use, classified in Class 536, subclass 27;

Claim 1 is generic, the first species is recited in claim 2 (a), and the following additional species are present:

- species 2, as recited in Claim 2 (b)
- species 3, as recited in Claim 3 (c)
- species 4, as recited in Claim 3 (d)
- species 5, as recited in Claim 3 (e)
- species 6, as recited in Claim 3 (f)
- species 7, as recited in Claim 3 (g)
- species 8, as recited in Claim 3 (h)
- species 9, as recited in Claim 7
- species 10, as recited in Claim 9
- species 11, as recited in Claim 10
- species 12, as recited in Claim 11
- species 13, as recited in Claim 12
- species 14, as recited in Claim 13
- species 15, as recited in Claim 14
- species 16, as recited in Claim 16
- species 17, as recited in Claim 17
- species 18, as recited in Claim 20
- species 19, as recited in Claim 21
- species 20, as recited in Claim 22
- species 21, as recited in Claim 23

Group II, claims 25-28, 31, and 32, drawn to polypeptides, classified in class 530, subclass 350.

Group III, claims 29, 30, 33, 34, 41, drawn to antibody compositions, classified in Class 530, subclass 207, and Class 435, subclass 5.

Group IV, claims 25-29, drawn to method using polypeptides, classified in Class 435, subclass 5.

Group V, claim 42, 43, 45, drawn to a vaccine, classified in class 424, subclass 89.

Group VI, Claim 44, drawn to a method of making a protein, classified in Class 530, subclass 350.

The claims of these six groups are drawn to distinct inventions which are not linked so as to form a single general inventive concept. PCT Rule 13.1 and 13.2 do not provide for multiple products and methods.

Attachment to PCT Telephone Memorandum for
Lack of Unity of Invention

5

Group I, Claims 1-24 and 40, drawn to DNA sequences, recombinant DNA, transformed host cell, and first method of use, classified in Class 536, subclass 27;

10

Claim 1 is generic, the first species is recited in claim 3 (a), and the following additional species are present:

15

species 2, as recited in Claim 3 (b)
species 3, as recited in Claim 3 (c)
species 4, as recited in Claim 3 (d)
species 5, as recited in Claim 3 (e)
species 6, as recited in Claim 3 (f)
species 7, as recited in Claim 3 (g)
species 8, as recited in Claim 3 (h)
species 9, as recited in Claim 7

20

species 10, as recited in Claim 9
species 11, as recited in Claim 10
species 12, as recited in Claim 11
species 13, as recited in Claim 12
species 14, as recited in Claim 13
species 15, as recited in Claim 14
species 16, as recited in Claim 16
species 17, as recited in Claim 17
species 18, as recited in Claim 20
species 19, as recited in Claim 21
species 20, as recited in Claim 22
species 21, as recited in Claim 23

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Group II, claims 25-28, 31, and 32, drawn to polypeptides, classified in class 530, subclass 350.

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Group III, claims 29, 30, 33, 34, 41, drawn to antibody compositions, classified in Class 530, subclass 387, and Class 435, subclass 5.

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Group IV, claims 35-39, drawn to method using polypeptides, classified in Class 435, subclass 5.

45

Group V, claim 42, 43, 45, drawn to a vaccine, classified in class 424, subclass 89.

Group VI, Claim 44, drawn to a method of making a protein, classified in Class 530, subclass 350.

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The claims of these six groups are drawn to distinct inventions which are not linked so as to form a single general inventive concept. PCT Rule 13.1 and 13.2 do not provide for multiple products and methods.